

85802

From: Jiang, Dong
Sent: Friday, January 31, 2003 7:16 PM
To: STIC-Biotech/ChemLib
Subject: 09/333,159

RECEIVED

FEB -3 2003

SEARCHED, SERIALIZED
(STIC)

Please search SEQ ID NO: 47

Please send results on paper to Dong Jiang in 10D-08 (mail stop CM1-10D19).
Thank you very much.

Dong Jiang (78243)
703-305-1345
U.S. Patent and Trademark Office
Art Unit 1646
dong.jiang@uspto.gov
CM1-10D08
Mail stop: CM1-10D19

Edward Hart
Technical Info. Specialist
STIC/Biotech
CMI 6B02 Tel: 305-9203

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 2/3/03
Date Completed: 2/3/03
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____ /
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: 02
WWW/Internet: _____
Other (specify): _____

Pending Nucleic Acid and/or Pending Amino Acid database searches now generate two sets of results. These databases were split into two parts to reduce the time needed to update the databases daily. The split freed up more machine time for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions, .rnpm and .rnpn

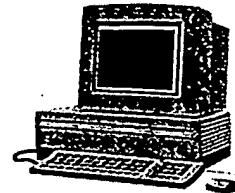
Searches run against the Amino Acid Pending database produce two sets of results, with the extensions, .rapm and .rapn

The Pending database search results should not be left in the case because they contain data that is confidential.

BioTech-Chem Library

Search Results

Feedback Form (Optional)



Scientific & Technical Information C

The search results generated for your recent request are attached. If you have any questions or comments (compliments or complaints) about the scope or the results of the search, please contact *the BioTech-Chem searcher* who conducted the search or contact:

Mary Hale, Supervisor, 308-4:
CM-1 Room 1E01

Voluntary Results Feedback Form

➤ *I am an examiner in Workgroup:* (Example: 1610)

➤ *Relevant prior art found, search results used as follows:*

- 102 rejection
- 103 rejection
- Cited as being of interest.
- Helped examiner better understand the invention.
- Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- Foreign Patent(s)
- Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ *Relevant prior art not found:*

- Results verified the lack of relevant prior art (helped determine patentability).
- Search results were not useful in determining patentability or understanding the invention

Other Comments:

Drop off completed forms at the Circulation Desk CM-1, or send to Mary Hale, CM1-1E01 or
mary.hale@uspto.gov

Copyright (c) 1993 - 2003 CompuGen Ltd.

GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: February 3, 2003, 13:48:09 ; Search time 18 Seconds
(without alignments)

Sequence: 1 MLENLSRQIVSHRMEMWLL.....IHLMQQEETNLSQLRCEAVL 423

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/podata/1/1aa/5A__COMB.pep:*

2: /cgn2_6/podata/1/1aa/5B__COMB.pep:*

3: /cgn2_6/podata/1/1aa/6A__COMB.pep:*

4: /cgn2_6/podata/1/1aa/6B__COMB.pep:*

5: /cgn2_6/podata/1/1aa/PCTUS_COMB.pep:*

6: /cgn2_6/podata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1282	57.1	392	4 US-09-820-001-4
2	1161	51.7	377	1 US-09-227-108-17
3	1161	51.7	377	2 US-09-073-674-17
4	150.5	51.2	379	1 US-09-227-108-18
5	150.5	51.2	379	2 US-09-073-674-18
6	1141.5	50.8	379	1 US-09-227-108-3
7	1141.5	50.8	379	2 US-09-073-674-3
8	1141.5	50.8	380	1 US-09-227-108-5
9	1141.5	50.8	380	2 US-09-073-674-5
10	1127	50.2	378	4 US-09-186-489-2
11	1098.5	48.9	380	1 US-09-227-108-16
12	1098.5	48.9	380	2 US-09-073-674-16
13	1031	45.9	395	4 US-09-820-001-2
14	105	45.7	430	1 US-09-484-105-22
15	105	4.7	430	1 US-09-484-106-22
16	102	4.5	346	2 US-09-602-359A-34
17	98.5	4.4	388	1 US-08-456-956-2
18	98.5	4.4	388	1 US-08-456-956-2
19	91	4.0	298	4 US-09-355-166-6
20	90	4.0	277	4 US-09-424-349A-6
21	89.5	4.0	624	2 US-08-756-317-9
22	89	4.0	494	4 US-09-134-001C-4475
23	89	4.0	494	2 US-08-968-542C-12
24	88.5	3.9	869	2 US-08-483-101-15
25	84.5	3.8	338	2 US-08-602-359A-40
26	84	3.8	935	1 US-07-707-367-2
27	84	3.7	370	4 US-09-222-938A-64

ALIGNMENTS

RESULT 1
US-09-820-001-4

Sequence 4, Appli
; Sequence 4, Application US/09820001
; Patent No. 638760

GENERAL INFORMATION:

APPLICANT: MERKULOV, Gennady et al

TITLE OF INVENTION: ISOLATED HUMAN LIPASE PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN LIPASE PROTEINS, AND USES THEREOF

FILE REFERENCE: CL001186

CURRENT APPLICATION NUMBER: US/09-820, 2001

CURRENT FILING DATE: 2001-03-29

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FASTSEQ for Windows Version 4.0

; SEQ ID NO 4
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Human
; US-09-820-001-4

Query Match 57.1%; Score 1282; DB 4; Length 392;
Best Local Similarity 63.8%; Pred. No. 5.1e-127;
Matches 234; Conservative 53; Mismatches 80; Indels 0; Gaps 0;

Qy 40 AVDPPEAFMNISEIIQHGYPCBEYEVATEDGILSVRIPRGIVQPKTGSRVPLQHG 99
Db 26 AVDPETNMNVEISIISWYGPSPSEYLVTEDEGYILCLNRPHGRKRNHSKDKGPKPWVFLHG 85
Qy 100 LVGGASNWISNLPNNSIGFLADAGFDVWMGNRSRGNNAWSRKHKLTSIDQEFWAFSYEM 159
Db 86 LLADSSSNWVTLANNSLGGFLADAGFDVWMGNRSRGNNTWSRKHKLTSQDEFWAFSYEM 145
Qy 160 ARFDPRAVINFLIQKIGQKTYVGYQGTTGKFTASTMPLEAKINMYFALAPIATR 219
Db 146 AKYDLPASINFLINKTGQEQVIVGHSGOTTGFFIASQIPELAKRIMFFALGPVASA 205
Qy 220 HAKSPSCKFLPDMKIGLCKKEFLYQTRFLRQLVYLCGIVDQVILDCSNTMLLGF 279
Db 206 FCTSPMAKLGRPLDHLIKDLEDFKELPQSAFLKWLGLTHVCTHILKELCGNLCPFLUGP 265
Qy 280 NTNMMNMRSASYAHTLAGSVQVNLIHWSQAVNSGEIRAFDNGSETKNEKCNQPTVVR 339
Db 266 NERNLNMRSVQYVTTSPAGTSVQNMHLHSQAVKFQFOADKGSSARNYFHNQSYPT 325
Qy 340 YVRDPMVPTAKWTFGGDLSLSPEDVKLSESTNLTKNTEWHDPTWGDAPHM 399
Db 326 YNVKDMVPTAVWGGHDWLADWVYDWNILLQITNLVHRESIPEWEHLDFWGLDAPWL 385
Qy 400 YNEIHL 406
|||||

386 YNKKINL 392

RESULT 2
S-08-227-108-17
Sequence 17, Application US/08227108
Patent No. 5807726

GENERAL INFORMATION:

APPLICANT: Blanchard, Claire
APPLICANT: Benicourt, Claude
APPLICANT: Junien, Jean-Louis
TITLE OF INVENTION: Recombinant Dog Gastric Lipase

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/227,108
FILING DATE: 03-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Fanucci, Allan A.
REGISTRATION NUMBER: 30,256
TELECOMMUNICATION INFORMATION:

TELEPHONE: 212 869-9864/9741
TELEX: 66141 PENNIE
TELEFAX: 212 869-9090

SEQUENCE CHARACTERISTICS:

LENGTH: 377 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

Query Match Score 51.7%; Best Local Similarity 57.7%; Pred. No. 3e-114; Length 377; Matches 213; Conservative 63; Mismatches 93; Indels 0; Gaps 0;

Y 42 DPEAFNINISEIQHQGPCEYEATEDGYISVNIRPGLYQPKKTGSRPVYVLLQHGLV 101
Y 102 GGASNTISLPNNSLGFITLADGFDTWGNRSRKHKTLSIDQDEFWAFSYDENAR 161
Y 9 NPEANNINISQMTVWYPCQCEYEVTTEDGYILGVYRIPHGKNNSENIGKPVYVLLQHGLI 68

b 69 ASATINVIANLPNNSLAFMLADGYDTWGLNSRGTNSWRKVVYSPDSYFWAFSDENAK 128

Y 162 FDLPAVINFLTQKGGKIIYVGSQDTGTMGETAFSTMPPELAOKIKMYFALAPATVKA 221
Y 129 YDLPATINFLVQKGGKIIYVGSQDTGTMGETAFSTPLAKKTKTYALAPATVYKT 188

b 222 KSPGTKFLLPDDMMKLGKKEFLKTRFLRVLVYLGQVILDQISNIMLGGFT 281
Y 189 QSPLKRKISFIPFLKLMFGKMMFLPHTYFDDFLGETCSREVLDLCSNTLEIFCGEIK 248

Y 282 NMNMRSAYVAHTLLAGTSVONILHQSQAVNSGELRAFDWGSSETKNIKCNOPTPVYR 341
Y 249 KNLNVSRFDVLLGHNPAGTSVODFLHQAOLVRSKQFQFNWGSQSPNMLHYNOKTPPEVD 308

Y 342 VRDMTYPATMGGDQDLNSPDEYKMLSEVNLYHKNIPEAHYDFTWGLDAPHMYN 401
Y 309 VSMATTPVAVNGNDLADPOVAMLPKLSNLLEHKELAINHLDFTWMDAQPQEYNN 368

RESULT 3
S-08-227-108-17
Sequence 17, Application US/09073674
Patent No. 598189

GENERAL INFORMATION:

APPLICANT: Blanchard, Claire
APPLICANT: Benicourt, Claude
APPLICANT: Junien, Jean-Louis
TITLE OF INVENTION: Recombinant Dog Gastric Lipase

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Warner Lambert Company
STREET: 2800 Plymouth Road
CITY: Ann Arbor
STATE: Michigan
COUNTRY: U.S.A.
ZIP: 48105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/073,674

ATTORNEY/AGENT INFORMATION:

NAME: Crissey, Todd M.
REGISTRATION NUMBER: 37,807
REFERENCE/DOCKET NUMBER: 5072-D1-66-TMC

TELECOMMUNICATION INFORMATION:

TELEPHONE: 734 622-7530
TELEFAX: 734 622-1553

TELEX:

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 377 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

Query Match Score 51.7%; Best Local Similarity 57.7%; Pred. No. 3e-114; Length 377; Matches 213; Conservative 63; Mismatches 93; Indels 0; Gaps 0;

Y 42 DPEAFNISIQLQHQGPCEYEATEDGYISVNIRPGLYQPKKTGSRPVYVLLQHGLV 101
Y 9 NPEANNINISQMTVWYPCQCEYEVTTEDGYILGVYRIPHGKNNSENIGKPVYVLLQHGLI 68

Db 102 GGASNTISLPNNSLGFITLADGFDTWGNRSRKHKTLSIDQDEFWAFSYDENAR 161
Db 69 ASATINVIANLPNNSLAFMLADGYDTWGLNSRGTNSWRKVVYSPDSYFWAFSDENAK 128

Y 129 YDLPATINFLVQKGGKIIYVGSQDTGTMGETAFSTPLAKKTKTYALAPATVYKT 188

b 222 KSPGTKFLLPDDMMKLGKKEFLKTRFLRVLVYLGQVILDQISNIMLGGFT 281
Db 189 QSPLKRKISFIPFLKLMFGKMMFLPHTYFDDFLGETCSREVLDLCSNTLEIFCGEIK 248

Y 282 NMNMRSAYVAHTLLAGTSVONILHQSQAVNSGELRAFDWGSSETKNIKCNOPTPVYR 341
Db 249 KNLNVSRFDVLLGHNPAGTSVODFLHQAOLVRSKQFQFNWGSQSPNMLHYNOKTPPEVD 308

Y 342 VRDMTYPATMGGDQDLNSPDEYKMLSEVNLYHKNIPEAHYDFTWGLDAPHMYN 401
Db 309 VSMATTPVAVNGNDLADPOVAMLPKLSNLLEHKELAINHLDFTWMDAQPQEYNN 368

Db 249 KNLNVSRFDVLLGHNPAGTSVODFLHQAOLVRSKQFQFNWGSQSPNMLHYNOKTPPEVD 308

Qy 342 VRDMTYPTAMTGGDMLSNPDEVKMLSEVTNLIYHKNIPEWAHDFTINGLDAPHMYN 401
 Db 309 VSAMTPAVANGGNDLADQDVAMLLPKLSNLFLHKEILAYNHLDFIWAMDAFQEVTN 368
 Qy 402 EIIHLMQE 410
 Db 369 EMISMAAE 377

RESULT 4
 US-08-227-108-18
 ; Sequence 18, Application US/08227108
 ; Patent No. 5807726
 ; GENERAL INFORMATION:
 ; APPLICANT: Blanchard, Claire
 ; APPLICANT: Benicourt, Claude
 ; APPLICANT: Junien, Jean-Louis
 ; TITLE OF INVENTION: Recombinant Dog Gastric Lipase
 ; NUMBER OF SEQUENCES: 21
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10016

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/227,108
 FILING DATE: 03-APR-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Fauci, Allan A.
 REGISTRATION NUMBER: 30,256
 REFERENCE/DOCKET NUMBER: 7620-033
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 790-9090
 TELEFAX: 212 869-8864/9741
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 379 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-227-108-18

Query Match 51.2%; Score 1150.5; DB 1; Length 379;
 Best Local Similarity 56.8%; Pred. No. 3.0e-113; Gaps 1;
 Matches 213; Conservative 65; Mismatches 94; Indels 3; Gaps 1;

Qy 37 PTVADPDAFMNISEIIHQGYCPEEYVATEGYIISVNIRPGLQKPKKGSRPVLL 96
 Db 7 PT---NPEVMNNSQMLSYWGPSEKEVYTEDGYIILEVNRLPYGKNSGNQRPVFL 63

Qy 97 QHGLVGLASNWISLPLNNSLGLFLIADQFDVWNGNSRENAWSRKHTLSIDODEFWAFSY 156
 Db 64 QHGLASASNWISLPLNNSLFLAFLADQGYWGNNSCQTSPRNLYSPDSVEFWAFS 123

Qy 157 DEMARFDLPAVINFILQTKGQEKIYVGYSQGTMGIFTASTMPELAQKIRMYFALAPIA 216
 Db 124 DEMARFDLPAVINFILQTKGQEKIYVGYSQGTMGIFTASTMPELAQKIRYFALAPIA 183

Qy 217 TVKAKSPOTKFLLPDMIKGJFGKSKFLYQTRFLRIVLQGQVILQDQCSNIMLL 276
 Db 184 TVKAKSPOTKFLLPDMIKGJFGKSKFLYQTRFLRIVLQGQVILQDQCSNIMLL 243

Qy 277 GGENTNNNNMSRASVYAAHTLAGTSVQNLHNSQAVNSGELRAFDWQSETKNEKCNOPT 336

Db 244 CGFDSDANLNMSRLDVYVSHNPAGTSVQNLHWTQAVKSGNQFAENNGSPAQNIVVHFNOPT 303
 Qy 337 PVR'RVDRMTVPTAMPTGGDMLSNPDEVKMLSEVTNLIYHKNIPEWAHDFTINGLDAF 396
 Db 304 PPYANTAMNPYAVGGNDLADQDVPLLPKLSNLFLHKEILYHNLDFIWAMNAP 363
 Qy 397 HRMNEIHLMQEE 411
 Db 364 QEVNTLISNMKDK 378

RESULT 5
 US-09-073-674-18
 Sequence 18, Application US/09073674
 Patent No. 5998189
 GENERAL INFORMATION:
 APPLICANT: Blanchard, Claire
 APPLICANT: Benicourt, Claude
 APPLICANT: Junien, Jean-Louis
 TITLE OF INVENTION: Recombinant Dog Gastric Lipase
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Warner-Lambert Company
 STREET: 2800 Plymouth Road
 CITY: Ann Arbor
 STATE: Michigan
 COUNTRY: U.S.A.
 ZIP: 48105
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/073,674
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Crissey, Todd M.
 REGISTRATION NUMBER: 37,807
 REFERENCE/DOCKET NUMBER: 5072-D1-66-TMC
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 734 622-7530
 TELEX:
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 379 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-09-073-674-18

Query Match 51.2%; Score 1150.5; DB 2; Length 379;
 Best Local Similarity 56.8%; Pred. No. 3.9e-113; Gaps 1;
 Matches 213; Conservative 65; Mismatches 94; Indels 3; Gaps 1;

Qy 37 PTKAVDPEAFMNISEIIHQGYCPEEYVATEGYIISVNIRPGLQKPKKGSRPVYLL 96
 Db 7 PT---NPEVMNNSQMLSYWGPSEKEVYTEDGYIILEVNRLPYGKNSGNQRPVFL 63

Qy 97 QHGLVGLASNWISLPLNNSLGLFLIADQFDVWNGNSRENAWSRKHTLSIDODEFWAFSY 156
 Db 64 QHGLASASNWISLPLNNSLFLAFLADQGYWGNNSCQTSPRNLYSPDSVEFWAFS 123

Qy 157 DEMARFDLPAVINFILQTKGQEKIYVGYSQGTMGIFTASTMPELAQKIRMYFALAPIA 216
 Db 124 DEMARFDLPAVINFILQTKGQEKIYVGYSQGTMGIFTASTMPELAQKIRYFALAPIA 183

Qy 217 TVKAKSPOTKFLLPDMIKGJFGKSKFLYQTRFLRIVLQGQVILQDQCSNIMLL 276
 Db 184 TVKAKSPOTKFLLPDMIKGJFGKSKFLYQTRFLRIVLQGQVILQDQCSNIMLL 243

Qy 277 GGENTNNNNMSRASVYAAHTLAGTSVQNLHNSQAVNSGELRAFDWQSETKNEKCNOPT 336

Qy	217	TVKHAKSPGTKEFLLLDDMMTIGLGFKEFLYQTRFRQ·LYTILGQVQDQICNSMILL	275
Db	184	TVKYETLNLKLMVPSFLKIGKIF·YPHFFDQFLATEVSRETVLCCSNALFI	242
Qy	276	LGGFNTNNMMSRASVYAAHTLAGTSQNTLHWSSQAVNSGELRAFDWGSETKLNKCNQP	335
Db	243	ICGFDTMNLNSRDLYDLSHAPAGTSQVNQVHWSQAVSGRFQADWGSPVQNMHRYHQ5	302
Qy	336	TPVRYRVRDMKVTPTAMMTGGDWLNSPVEDYKMLLSSEVTNLIYHKNIKPEWAHVDETLGDLA	395
Db	303	MPPYXNLTDMHVPIAVWNGNDLLADPHDYDVLSSKLPLNLYHKRIPPYNHLDFTWAMDA	362
Qy	396	PHRMYNELIHEM 407	
Db	363	PQAVYNEIVSHM 374	
RESULT 7			
	US-09-073-674-3	Sequence 3 Application US/09073674	
	Patent No. 5938189		
	GENERAL INFORMATION:		
	APPLICANT: Blaichard, Claire		
	APPLICANT: Penicourt, Claude		
	APPLICANT: Junien, Jean-Louis		
	TITLE OF INVENTION: Recombinant Dog Gastric Lipase		
	NUMBER OF SEQUENCES: 21		
	CORRESPONDENCE ADDRESS:		
	ADDRESSEE: Warner-Lambert Company		
	STREET: 2800 Plymouth Road		
	CITY: Ann Arbor		
	STATE: Michigan		
	COUNTRY: U.S.A.		
	ZIP: 48105		
	COMPUTER READABLE FORM:		
	MEDIUM TYPE: Floppy disk		
	COMPUTER: IBM PC compatible		
	OPERATING SYSTEM: PC-DOS/MS-DOS		
	SOFTWARE: Patent in Release #1.0, Version #1.25		
	CURRENT APPLICATION DATA:		
	APPLICATION NUMBER: US/09/073,674		
	FILING DATE:		
	CLASSIFICATION:		
	ATTORNEY/AGENT INFORMATION:		
	NAME: Crissey, Todd M.		
	REGISTRATION NUMBER: 37,807		
	REFERENCE/DOCKET NUMBER: 5072-D1-66-TMC		
	TELECOMMUNICATION INFORMATION:		
	TELEPHONE: 734 622-7530		
	TELEFAX: 734 622-1553		
	TELEX:		
	INFORMATION FOR SEQ ID NO: 3:		
	SEQUENCE CHARACTERISTICS:		
	LENGTH: 379 amino acids		
	TYPE: amino acid		
	TOPOLOGY: linear		
	MOLECULE TYPE: protein		
	US-09-073-674-3		
	Query Match 50.8%; Score 1141.5; DB 2; Length 379;		
	Best Local Similarity 56.5%; Pred. No. 3,4e-112; Mismatches 90; Indels 5; Gaps 63		
Qy	37	PTKAVDPEAFMNISEIIOHQGYPCEYEVATEDGYILSVNRPGRQYQPKKTGSPRVILL	96
Db	7	PT---NPEVTMISQMTYWGPAEEEVYDGYILGIDIPYGRNSENJGRVRAFL	63
Qy	97	QHGLGGASNWISNLPNNSLGFILADGEDYWMGNSRGNMSRKHTLSDQDEFWAFSY	156
Db	64	QHGLLASATWNSNPLNSLAFIADGYDWLNSRGNTRWANLYSPDSVEFWAFSF	123
Qy	157	DEMARFDPAVINFORTQKQIYIYGGSGTMMGJAFSTMPLEQAKIMYFALAPIA	

RESULT 8

US-08-227-108-5

Sequence 5, Application US/08227108

Patent No. 5607726

GENERAL INFORMATION:

APPLICANT: Blanchard, Claire

APPLICANT: Banicourt, Claude

APPLICANT: Junien, Jean-Louis

TITLE OF INVENTION: Recombinant Dog Gastric Lipase

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Penne, F. Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/227,108

FILING DATE: 03-APR-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Fanucci, Allan A.

REGISTRATION NUMBER: 30,256

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212 869-9050

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 380 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-227-108-5

Query Match 50.8%; Score 1141.5; DB 1; Length 380;

Best Local Similarity 56.3%; Pred. No. 3.5e-112; Length 380;

Matches 210; Conservative 67; Mismatches 90; Indels 5; Gaps 3;

Qy 37 PTKAVDPEAPMNISEIIOHQGCPBEYATEDGYILSYNRIPRLQPKKTGSRPVVLL 96

Db 8 PT--NPEVTMNISQMTIYTQPAEEVYTEDGYILGIDRIPYGRKNSNIGRPPVAFL 64

Qy 97 QHGLYGGASWNISLNLPNSLGFILADAGFDWGNNSRGNASRKHKTLSIDQDEFWAFSY 156

Db 65 QHGLLASATWNISLNLPNSLAFILADAGDYLGNISRGNTWARRNLXSPDSVEWAFSF 124

Qy 157 DEMARYDLPATIDFILKTKGQDKLHYVGHQSQTTIGFAESTNPKLAKRKTFYALAVIA 183

Db 125 DEMARYDLPATIDFILKTKGQDKLHYVGHQSQTTIGFAESTNPKLAKRKTFYALAVIA 184

Qy 217 TVKHAKSPTKTFKLPLDMMIKGLFGKKEIYQORFLRQ-LVIVLGQVILDQICSNIML 275

Db 184 TVK/TETLNLKMLVPSFLKLFGNKF-YPHHFFDQFLATEVCSRETVDLCSNALFI 242

Qy 276 LGGFNTNNRNMRSASVYAAHTLAGTSVONLHWSQAVNSGELRAFDWSESETKNELEKCNQP 335

Db 243 ICGFDTMNLNMSRLDVLHNPAGTSVONLHWSQAVNSGKFAQDWSSPVQNMHHYQS 302

Qy 336 TPVRYRVRDMTVPAMWGTGQDWLSNPEDYKMLUSEVNTNLHYKRNIPWAHYDFTWGLDA 395

Db 303 MPYXNLTDMHVPIAVWNGNDLADPHDVLSSKLPLNLYHRRKIPPNHLDIWANDA 362

Qy 396 PHMYNEITHLM 407

Db 363 PQAVYEVSSM 374

Db 364 PQAVYEVSSM 375

RESULT 9

US-09-073-674-5

Sequence 5, Application US/09073674

Patent No. 5998189

GENERAL INFORMATION:

APPLICANT: Blanchard, Claire

APPLICANT: Benicourt, Claude

APPLICANT: Junien, Jean-Louis

TITLE OF INVENTION: Recombinant Dog Gastric Lipase

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Warner-Lambert Company

STREET: 2880 Plymouth Road

CITY: Ann Arbor

STATE: Michigan

COUNTRY: U.S.A.

ZIP: 48105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/073,674

FILING DATE: 05-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Crissey, Todd M.

REGISTRATION NUMBER: 37,807

REFERENCE/DOCKET NUMBER: '507-2-DI-66-TMC

TELECOMMUNICATION INFORMATION:

TELEPHONE: 734 622-7530

TELEFAX: 734 622-1553

TELEFAX:

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 380 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-073-674-5

Query Match 50.8%; Score 1141.5; DB 2; Length 380;

Best Local Similarity 56.3%; Pred. No. 3.5e-112;

Matches 210; Conservative 67; Mismatches 90; Indels 5; Gaps 3;

Qy 37 PTKAVDPEAPMNISEIIOHQGCPBEYATEDGYILSYNRIPRLQPKKTGSRPVVLL 96

Db 8 PT--NPEVTMNISQMTIYTQPAEEVYTEDGYILGIDRIPYGRKNSNIGRPPVAFL 64

Qy 97 QHGLYGGASWNISLNLPNSLGFILADAGFDWGNNSRGNASRKHKTLSIDQDEFWAFSY 156

Db 65 QHGLLASATWNISLNLPNSLAFILADAGDYLGNISRGNTWARRNLXSPDSVEWAFSF 124

Qy 97 QHGLYGGASWNISLNLPNSLGFILADAGFDWGNNSRGNASRKHKTLSIDQDEFWAFSY 156

65 QHGILLASATNWISLNPNNSLAFILADAGYDVWLGNSRQNTWARRNLKYSQPSVETWAFSF 124
 QY 157 DEMARFDIPAVINFLQKTKQEKIYKYYGYSQGTMTGFLAFTSMPELAQKIKMYFALAPTA 216
 Db 125 DEMAKYDIPATIDFLKTKQDKHKKHYSQGTIGFTAFSTNFKLAKRKKTYALAPTA 184
 QY 217 TVKHAKSPTKFLLPDMKIKLGFKKEFLYQTRFLRQ_LVIVLGQVILDQFCNSNIMLL 275
 Db 185 TVKYEETLNKLMVPSFLKFLGKNLIF-YPHFFDQFLATECSRETVLCSNALPFI 243
 QY 276 LGGENTNNNNMSRASVYAAHTLAGTSVQNTLHNSQAVNSGELRAFDWGSSETKNLKCNPQ 335
 Db 244 ICGFDTMNLNMSRLDVLSHNPAGTSVQNLHNSQAVSKGKFQFDWGSQVNMHYHQS 303
 QY 336 TVPVRVDRDVTPTAMWTCGQDNLNSNPEDYKMLJSEVTNLIYHKNIPEWAHDFIWGLDA 395
 Db 304 MPPYNTLDMHVPJAVWNGNDLLADPHDVLLSLKPNLJYHRKIPPYNHLDFTIWMDA 363
 QY 396 PHRMYNEITHM 407
 Db 364 PQAVYNEITSM 375

RESULT 10
 sequence 2, Application US/09186489
 ; Patent No. 6375947
 ; GENERAL INFORMATION:
 ; APPLICANT: Bolen, Paul L.
 ; APPLICANT: Cihak, Paul L.
 ; APPLICANT: Sharp Jr., Lewis G.
 ; TITLE OF INVENTION: Purified Recombinant Kid Pregastric Esterase, and
 ; TITLE OF INVENTION: Processes for its Production and Use
 ; FILE REFERENCE: 5499/2
 ; CURRENT APPLICATION NUMBER: US/09/186,489
 ; CURRENT FILING DATE: 1998-11-05
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO: 2
 ; LENGTH: 378
 ; TYPE: PRT
 ; ORGANISM: Kid (Goat)
 ; US-09-186-489-2

Query Match Score 1127; DB 4; Length 378.
 Best Local Similarity 55.1%; Pred. No. 1.2e-110; Indels 0; Gaps 0;
 Matches 205; Conservative 66; Mismatches 101; Indels 0; Gaps 0;

Query Match Score 1098.5; DB 1; Length 380;
 Best Local Similarity 54.6%; Pred. No. 1.2e-107; Indels 1; Gaps 1;
 Matches 202; Conservative 69; Mismatches 98; Indels 1; Gaps 1;

Qy 40 AVDPBAFMNSETIIOHQGYPEEYEVATEDGYIISYNRIPRGLYQPKKTGSRPVYLLQHG 99
 Db 6 AKNPBASMYNQMSFWGPSEMHRVITADGYIQLQYRIPHGKDNDHHLGQRPVYFLQHG 65

Qy 100 LVGGGSNWSLNPNNSLGFILADAGFDWGNNSRQNAWSKHKHTS1DQDFEWASYDEM 159
 Db 66 LLASATNWISLNPNNSLGFILADAGFDWGNNSRQNTWAQHLYSPDSEFWASFDEM 125

Qy 160 ARFDPAVINFLQKTKQEKIYKYYGYSQGTMTGFLAFTSMPELAQKIKMYFALAPTA 219
 Db 126 AEYDFSTIDFLKQKHHYSQGTIGFTAFSTNPLAETEYPHALAPTAVK 185

Qy 220 HAKSPGTKEFLLPDMKIKLGFKKEFLYQTRFLRQVILCQGQVILDQICSNIMLLGGF 279
 Db 186 HTQSLFNKLALIPHFLKIFGKNAFYPHNFFEQFLGVECSRETDVLCKRNALPAITGA 245

Qy 280 NTNNNNMSRASVYAAHTLAGTSVQNTLHNSQAVNSGELRAFDWGSSETKNLKCNPQTPV 339
 Db 246 DNKNFNMMSRLDYYVHNPGASVQNLHWAQSKFQFDWGSQVNLHMYHNPQTPPI 305

Qy 340 YRVDRTVPTAMWTCGQDWLNPEDKM1SEVTNLIYHKNIPEWAHDFIWGLDAPHRM 399
 Db 306 YNLTAMNPVIAWSQGDLIADPDQVYDILLSKLSNLHKEIPNWNHLDFTWAMDRPQE 365

Qy 400 YNEITHM0QEE 411

APPLICANT: MCNALLY, Francis J
 APPLICANT: LAURENSON, Patricia
 APPLICANT: HERSKOWITZ, Ira
 APPLICANT: LI, Joachim J
 APPLICANT: GAVIN, Kimberly
 TITLE OF INVENTION: ORIGIN OF REPLICATION COMPLEX GENES
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESS: FLEIR, HOHBACH, TEST, ALBRITTON & HERBERT
 STREET: 4 Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-4187
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/484,105
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Osman Ph.D., Richard Aron
 REGISTRATION NUMBER: 36 627
 REFERENCE/DOCKET NUMBER: A-59032/DJB/RAO
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 494-8700
 TELEFAX: (415) 494-8771
 TELEX: 910 277299
 INFORMATION FOR SEQ ID NO: 22:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 430 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-484-105-22

Query Match 4.7%; Score 105; DB 1; Length 430;
 Best Local Similarity 21.9%; Pred. No. 0.016; Gaps 13;
 Matches 61; Conservative 42; Mismatches 87; Indels 88; Gaps 13;

Qy 85 PPKIGSRPVVLQHGLGGASNINSNLPPN-----SLGF-----ILADAGFDW--MGN 131
 Db 25 PEGESR-----QKTKTKENASRNLSNLNEEDLEQIISFEDEVSNM-----SLGF-----ILADAGFDW--MGN 131
 Qy 132 S---RGNAWSRKH-----TLSIDQDEFWAFSYDEMARFDLPAVINFIQTKQERKTY 181
 Db 79 SASERMNNAKSRRRAGNGNTTEEDDEDEISNAITDFTKCDLPLRNYYITKADNTFEK 138
 Qy 182 YVGQSQTGMGFIASFSTMPLEAKTIVKMFALAPATVKAHSPTKFLLPDMIKLFG 241
 Db 139 RLEFLADNDFG-----KWKLLAAG-----FNLHGYGS 168
 Qy 242 KKEFLYOTRFLRQVYLQGQVILQDQCSNIMLIGGENTN--NMNMSRASYAAHTLA 298
 Db 169 KRDVL-TFENELSDYTMVRDQKDGIVKVLGA;NENMKLNCKNYKRG-----217
 Qy 299 GTSYONILHWSQAV---NSGEL-----RAFDWSE 325
 Db 218 ---QSTISWARSIRRKMSQQLLIIIDNIEAPWRSRSD 251

Query Match 4.7%; Score 105; DB 1; Length 430;
 Best Local Similarity 21.9%; Pred. No. 0.016; Gaps 13;
 Matches 61; Conservative 42; Mismatches 87; Indels 88; Gaps 13;

Qy 85 PPKIGSRPVVLQHGLGGASNINSNLPPN-----SLGF-----ILADAGFDW--MGN 131
 Db 25 PEGESR-----QKTKTKENASRNLSNLNEEDLEQIISFEDEVSNM-----SLGF-----ILADAGFDW--MGN 131
 Qy 132 S---RGNAWSRKH-----TLSIDQDEFWAFSYDEMARFDLPAVINFIQTKQERKTY 181
 Db 79 SASERMNNAKSRRRAGNGNTTEEDDEDEISNAITDFTKCDLPLRNYYITKADNTFEK 138
 Qy 182 YVGQSQTGMGFIASFSTMPLEAKTIVKMFALAPATVKAHSPTKFLLPDMIKLFG 241
 Db 139 RLEFLADNDFG-----KWKLLAAG-----FNLHGYGS 168
 Qy 242 KKEFLYOTRFLRQVYLQGQVILQDQCSNIMLIGGENTN--NMNMSRASYAAHTLA 298
 Db 169 KRDVL-TFENELSDYTMVRDQKDGIVKVLGA;NENMKLNCKNYKRG-----217
 Qy 299 GTSYONILHWSQAV---NSGEL-----RAFDWSE 325
 Db 218 ---QSTISWARSIRRKMSQQLLIIIDNIEAPWRSRSD 251

RESULT 15
 US-08-484-106-22
 Sequence 22, Application US/08484106
 Patent No. 5614618
 GENERAL INFORMATION:
 APPLICANT: STILLMAN, Bruce
 APPLICANT: BELL, Stephen P
 APPLICANT: KOBAYASHI, Ryuji
 APPLICANT: RINE, Jasper

Search completed: February 3, 2003, 13:50:50
 Job time : 19 secs

4 protein - protein search, using sw model										
run on: February 3, 2003, 13:44:29 ; Search time 40 Seconds (without alignments); 1409.125 Million cell updates/sec										
title:	US-09-333-159-47									
pref. score:	2247									
sequence:	1 MLETLSRQATVSHRMWNL.....IHLMQQEETNLSQLRCEAVYL 423									
scoring table:	BLOSUM62									
gapop:	10.0 , Gapext. 0.5									
searched:	908470 seqs., 13250620 residues									
Total number of hits satisfying chosen parameters: 908470										
Minimum DB seq length: 0										
Maximum DB seq length: 2000000000										
Post-processing: Minimum Match 0%										
Maximum Match 100%										
Listing first 45 summaries										
Database :										
A_Geneseq.101002:*										
1:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*									
2:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*									
3:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*									
4:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*									
5:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*									
6:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*									
7:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*									
8:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*									
9:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*									
10:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*									
11:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*									
12:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*									
13:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*									
14:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*									
15:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*									
16:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*									
17:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*									
18:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*									
19:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*									
20:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*									
21:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*									
22:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*									
23:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*									
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.										
SUMMARIES										
result No.	Score	Query Match	Length	DB ID	Description					
1	2247	100.0	423	22 AAB66065	Human TANGO 294					
2	2174	96.8	409	22 AAE11931	Human CG162 (or					
3	2076	92.4	390	22 AAB66074	Human TANGO 294					
4	1991	88.6	398	23 AAU93164	Human lysosomal					
5	1536.5	68.4	371	23 AAU93165	Human shear stre					
6	1289	57.4	399	22 AAB660783	Human lysosomal					
7	1289	57.4	399	22 AAB66061	Human lysosomal					
8	1282	57.1	392	23 AAQ18227	Human lysosomal					
9	1191.5	53.0	398	22 AAB660498	Novel, human secr					
10	1166	51.9	398	14 AAR31302	RGT precursor					

Human TANGO 294 ex		Human TANGO 294		Human TANGO 294	
11	11163	51.8	221	22	AAB66688
11	11567	51.5	395	6	AAP50312
12	11567	51.9	395	23	AAE14144
13	11143	50.9	399	23	AAU77496
14	11143	50.9	379	15	AAR56170
15	11413	50.8	379	17	AAW0982
16	11413	50.8	380	15	AAR56171
17	11413	50.8	399	22	AAG6713
18	11133	50.7	403	23	AAU77493
19	11135	50.6	427	23	AAE17308
20	11119	49.8	397	23	ABB76189
21	11119	49.8	378	23	AAP60724
22	11119	49.8	398	7	AAP60688
23	11119	49.8	398	17	AAW0983
24	11119	49.8	398	22	AAB66886
25	11101	49.0	1090	48.5	AAU98339
26	10901	48.5	1031	45.9	AAO18226
27	10901	45.9	977	43.5	AAE17107
28	977	43.5	977	40.4	AEE14146
29	977	40.4	731	34.8	144
30	783	34.8	731	34.8	22
31	781	34.8	276	34.8	22
32	777	34.6	289	34.6	23
33	745.5	33.2	280	32.2	23
34	724.5	32.2	656	22	ABG26839
35	691	30.8	233	22	AAB61508
36	663	29.5	394	22	ABB71102
37	655.5	29.2	434	22	AAB62081
38	639	28.4	456	22	ABH65957
39	636	28.3	398	22	ABB63011
40	627	27.9	311	23	AAU98440
41	598.5	26.2	838	22	ABB61967
42	567.5	25.3	457	22	ABB63187
43	559	24.9	399	22	ABB71142
44	546	24.3	439	22	ABB63143
45	535	23.8	416	22	ABB59328

Homo sapiens.
WO200077239-A2.
21-DEC-2000.
24-MAY-2000; 2000
14-JUN-1999;
(MILL-) MILLENNIUM
McCarthy SA, F
WPI; 2001-03231
N-PENDR. AFRA4513

XX TANGO and INTERCEPT nucleic acids, proteins, and antibodies, useful for screening assays and diagnostic assays and for the treatment of neurological diseases such as Alzheimer's, Parkinson's and Huntington's disease.

XX Claim 8; Fig 6; 359pp; English.

PS The present invention relates to TANGO or INTERCEPT proteins and coding sequences (see AAF45121-445136 and AAF45138-F45139 and AAB65031-B66057, AAB66064-B66083 and AAB66085). The TANGO/INTERCEPT proteins and coding sequences are useful for the treatment of neurological disorders such as central nervous system (CNS) disorders, CNS-related disorders, focal brain disorders, global diffuse cerebral disorders and other neurological and cerebrovascular disorders. The CNS disorders include Alzheimer's disease, senile dementia, Huntington's disease, amyotrophic lateral sclerosis, Parkinson's, Gilles de la Tourette's syndrome, autonomic function disorders such as hypertension and sleep disorders, neuropsychiatric disorders, psychoactive substance use disorders, anxiety, and bipolar affective disorder.

XX Sequence 423 AA:

Query Match 100.0%; Score 2247; DB 22; Length 423; Best Local Similarity 100.0%; Pred. No. 8.5e-220; Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLETLSROWTSHRMEMWLLVAVMFQRNVNSVHMPPTKAVDPEAFMNISEIIQHOGYPC 60
Db 1 MLETLSROWTSHRMEMWLLVAVMFQRNVNSVHMPPTKAVDPEAFMNISEIIQHOGYPC 60

Qy 61 EEEYATEDGVLTSWRIPRGLVQPKKTTGSRPVLVQHGLYGGASWNIWNPNNSLGFIL 120
Db 61 EEEYATEDGVLTSWRIPRGLVQPKKTTGSRPVLVQHGLYGGASWNIWNPNNSLGFIL 120

Qy 121 ADAGFDYWMGNSRGNAWSRKRHTLSDQDEFWAFSYDEMARFDLPAVINFQKQGEKI 180
Db 121 ADAGFDYWMGNSRGNAWSRKRHTLSDQDEFWAFSYDEMARFDLPAVINFQKQGEKI 180

Qy 181 YYGVYSGTGTNGFIASTMPLEAQLKIRKMYFALIAPATVKHAKSPGTFKFLLPDMMIKGLF 240
Db 181 YYGVYSGTGTNGFIASTMPLEAQLKIRKMYFALIAPATVKHAKSPGTFKFLLPDMMIKGLF 240

Qy 241 GKKFELYQTRFLQYLTLCGQVILQDICSNTMLLGGFTNTNNMMSRASYAAHTLAGT 300
Db 241 GKKFELYQTRFLQYLTLCGQVILQDICSNTMLLGGFTNTNNMMSRASYAAHTLAGT 300

Qy 301 SVQNLIHWSQAVNSGELRAFDGSETKNLCKNQPTPVRVDRDMVPTAMWTGGDWL 360
Db 301 SVQNLIHWSQAVNSGELRAFDGSETKNLCKNQPTPVRVDRDMVPTAMWTGGDWL 360

Qy 361 NPEDVRLMSEVTNLIYHKNIPWAHYDFINGLDAPIHMRMYNEIIHLMQQEETNLSGRC 420
Db 361 NPEDVRLMSEVTNLIYHKNIPWAHYDFINGLDAPIHMRMYNEIIHLMQQEETNLSGRC 420

Qy 421 AVL 423
Db 421 AVL 423

RESULT 2
AAE11931 standard; Protein; 409 AA.

XX ID AAE11931; AC AAE11931; DT 18-DEC-2001 (first entry)
XX DE Human CG162 (or C59) lipase protein #2.
XX Human: apolipoprotein; lipase; lipoprotein receptor; Alt: angina; cardiovascular disease; lipid metabolism; myocardial infarction; cerebral ischaemia; arterial thrombosis; thrombolytic; antihaemiac;

KW coronary artery thrombosis; cerebral artery thrombosis; stroke; intracardiac thrombosis; gene therapy; cardiovascular; vasodilator; neuroprotectant; cerebroprotective.

XX OS Homo sapiens.

XX Key Peptide PH Location/Qualifiers 1.19
XX FT /label= Signal_peptide
XX Protein FT 20..409
XX /note= "Human mature CG162 (or C59) lipase protein"
XX WO200179446-A2.
XX PN 25-OCT-2001.
XX PD 25-OCT-2001.
XX PF 16-APR-2001; 2001W0-US12529.
XX PA (HYSEQ INC.
XX PI Ballinger DG, Loeb D, Montgomery JR, Tang TY, Zhou P, Goodrich R; Liu C, Asundi V, Zhao Q, Wehrman T, Drmanac RT, Ren F, Qian X; Wang D;
XX PI Liu C, Asundi V, Zhao Q, Wehrman T, Drmanac RT, Ren F, Qian X; Wang D;
XX DR WPI; 2001-611724/70.
XX DR N-PSDB; AA19226.
XX PT Nucleic acids encoding human apolipoproteins, lipases, and lipoprotein receptor polypeptides, useful for preventing diagnosing and treating lipid metabolism disorders, thrombosis and cardiovascular diseases.
XX CLA 10: Fig 3: 266pp; English.
XX PS The invention relates to polynucleotides encoding proteins CG122, CG179, CG95, CG121, CG162, CG27, CG153 and CG168 which are related to proteins involved in lipid metabolism and cardiovascular disease, such as human apolipoproteins, lipases and lipoprotein receptor proteins. These DNA and protein sequences are useful for treating or preventing disorders associated with apolipoproteins, lipases and lipoprotein receptor (ALR) expression and for treating lipid metabolism, cardiovascular diseases and thrombosis. Antibodies against these proteins are useful for determining the presence of or predisposition to a disease associated with altered levels of these sequences. ALR polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them and cells expressing ALR proteins. These DNA and protein sequences are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of this polypeptide. Vectors comprising these DNA and protein sequences are also useful for producing ALR proteins. The nucleic acids and polypeptides of the invention are also useful for the treatment of occlusive cardiovascular diseases, myocardial infarction, cerebral ischaemia, angina, arterial thrombosis, coronary artery thrombosis and cerebral artery thrombosis or intracardiac thrombosis and stroke. The nucleotides of the invention are used in gene therapy. The present sequence is human CG162 (or C59)
XX Sequence 409 AA:
Query Match 96.8%; Score 2174; DB 22; Length 409; Best Local Similarity 100.0%; Pred. No. 2.2e-22; Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 15 MEMWLLVAVMFQRNVNSVHMPPTKAVDPEAFMNISEIIQHOGYPCFEYATEDGYILS 74
Db 1 M EMWLLVAVMFQRNVNSVHMPPTKAVDPEAFMNISEIIQHOGYPCFEYATEDGYILS 60
Qy 75 VNRIPRGLVQPKRTGSRPVLLQHGLYGGASWNIWNPNNSLGFILADAGGDFVWGNNSRG 134

Db	61	VNRIPRGVQPKKTSRPPVLLQGLGGASNWISNLPNNSLGTIADAGEDFTMGNRG	120	CC autonomic function disorders such as hypertension and sleep disorders, CC neuropsychiatric disorders, psychoactive substance use disorders, CC anxiety, and bipolar affective disorder.
Qy	135	NAWSRKHTKLSIDQDEFWAFSYDEMARFDLPAVINFILOKTKQEQEYIYGGYSQGTTMGMFI	194	XX
Db	121	NAWSRKHTKLSIDQDEFWAFSYDEMARFDLPAVINFILOKTKQEQEYIYGGYSQGTTMGMFI	180	XX
Qy	195	AESTNPELAQOKIYMFALAPATIYKHKASPGTCKLPPDMMIKSLFGKEFLYOTRFLRQ	254	XX
Db	181	AESTNPELAQOKIYMFALAPATIYKHKASPGTCKLPPDMMIKSLFGKEFLYOTRFLRQ	240	XX
Qy	255	LVIYLGQVLDQICSNIMLLGGENTNNMSRASYVAHTLAGTSVNILHKSQAVNS	314	Sequence 390 AA;
Db	301	GELRAFDWGSETKNEKCKNQOPTPYVRDMTPTAMTGGQDWLNSNPEDVKMILSEVTN	374	Query Match 92.4%; Score 2076; DB 22; Length 390;
Db	241	LVIYLGQVLDQICSNIMLLGGENTNNMSRASYVAHTLAGTSVNILHKSQAVNS	300	Best Local Similarity 100.0%; Pred. No. 1.9e-202; Indels 0; Gaps 0;
Qy	315	GELRAFDWGSETKNEKCKNQOPTPYVRDMTPTAMTGGQDWLNSNPEDVKMILSEVTN	374	Matches 390; Conservation 0; Mismatches 0;
Db	301	GELRAFDWGSETKNEKCKNQOPTPYVRDMTPTAMTGGQDWLNSNPEDVKMILSEVTN	360	QY 34 VHMPTKAVDPEAFMNISEILOHQGPCEEEYEVATEDGYIILSVNRIIPRGLVQPKTKGSRPV 93
Db	241	LVIYLGQVLDQICSNIMLLGGENTNNMSRASYVAHTLAGTSVNILHKSQAVNS	300	Db 1 VHMPTKAVDPEAFMNISEILOHQGPCEEEYEVATEDGYIILSVNRIIPRGLVQPKTKGSRPV 60
Qy	375	LIVHKNIPENAHVDEFTWGLDAPHMYNEIILHMQEETNLNSQGRCEAVL	423	QY 94 VLIQGLVGASNWISNLPNNSLGPFLADAGFDWGNNSRGNAWSRKHKTLISIDQDEFWA 153
Db	361	LIVHKNIPENAHVDEFTWGLDAPHMYNEIILHMQEETNLNSQGRCEAVL	409	Db 61 VLIQGLVGASNWISNLPNNSLGPFLADAGFDWGNNSRGNAWSRKHKTLISIDQDEFWA 120
RESULT 3				QY 154 FSYDEMAREFDLPAVINFILOKTKQEQEYIYGGYSQGTTMGMFIATSTMPMELAQOKIYMFAL 213
AAB66067	1D	AAB66067 standard; Protein: 390 AA.		Db 121 FSYDEMAREFDLPAVINFILOKTKQEQEYIYGGYSQGTTMGMFIATSTMPMELAQOKIYMFAL 180
AC				QY 214 PIATVYKAKSPGTKEFLPDMMIKSLFGKEFLYQTRFLQVLYLGQVILDQICSNIM 273
XX				Db 181 PIATVYKAKSPGTKEFLPDMMIKSLFGKEFLYQTRFLQVLYLGQVILDQICSNIM 240
DT				QY 274 LLIGGENTNNMSRASYVAHTLAGTSVNILHNSQAVNSGEIARFDWGSETKNEKCN 333
XX				Db 241 LLIGGENTNNMSRASYVAHTLAGTSVNILHNSQAVNSGEIARFDWGSETKNEKCN 300
XX				QY 334 QPTPYRYVRDMTPTAMTGGQDWLNSNPEDVKMILSEVTNLYHKNPENAHVDFIWGL 393
XX				Db 301 QPTPYRYVRDMTPTAMTGGQDWLNSNPEDVKMILSEVTNLYHKNPENAHVDFIWGL 360
DE				QY 394 DAPHMYNEIILHMQEETNLNSQGRCEAVL 423
XX				Db 361 DAPHMYNEIILHMQEETNLNSQGRCEAVL 390
				RESULT 4
				AAU99164
				ID AAU99164 standard; Protein: 398 AA.
				XX
				AC AAU99164;
				XX
				DT 24-SEP-2002 (first entry)
				XX
				DE Human lysosomal acid lipase #1.
				XX
				KW Human: enzyme; lysosomal acid lipase; lipid malabsorption illness;
				KW cystic fibrosis; alcoholism; heart disease; heart attack;
				KW Wolman disease; cholesterol ester storage disease; brain injury;
				KW mood disorder; anxiety disorder; thought disorder; volition disorder;
				KW sleep disorder; nerogenic disorder; myopathic disorder; CPD;
				KW obesity; cancer; chronic obstructive pulmonary disease; diabetes;
				KW cardiovascular disorder; Alzheimer's disease; Parkinson's disease;
				KW anorexia; osteoarthritis; Alzheimer's disease; Parkinson's disease;
				XX peripheral nervous system disorder.
				XX Homo sapiens.
				XX WO200236731-A2.
				XX PN
				XX PD 10-MAY-2002.
				XX PP 30-OCT-2001; 2001WO-EP12518.
				XX PR 31-OCT-2000; 2000US-244170P.
				XX PR 29-MAY-2001; 2001US-293516P.
				PA (FARB) BAYER AG.
				XX Xiao Y;

XX	DR	WPI: 2002-1519248/55	DE	Human lysosomal acid lipase #2.
XX	DR	N-PSDB; ABK86569.		
XX	PT	Novel human lysosomal acid lipase polypeptide, useful for treating cancer, diabetes, obesity, chronic obstructive pulmonary disease, peripheral or central nervous system disorder or cardiovascular disorder.		
XX	PT	Claim 25; Fig 2; 126pp; English.		
CC	CC	The invention relates to a purified human lysosomal acid lipase polypeptide. Also included are the polynucleotide encoding the lipase (or its fragment, derivative, allele or sequence at least 60% identical to it), vectors, host cells, a reagent (e.g. an antisense oligonucleotide) which binds to the lipase or polynucleotide (used for detection and modulating/reducing the lipase activity) and an anti-lipase antibody. The lipase and polynucleotide are useful for identifying therapeutic agents that either increase or decrease the lipase activity. The identified agent, the lipase and polynucleotide are useful for treatment of a disease such as lipid malabsorption illness, cystic fibrosis, alcoholism, heart disease, heart attack, Wolman disease, cholesterol ester storage disease, brain injury, mood disorder, anxiety disorder, thought disorder, volition disorder, sleep disorder, neurogenic disorder, myopathic disorder, obesity, cancer, chronic obstructive pulmonary disease (COPD), diabetes, cardiovascular disorder, Alzheimer's disease, Parkinson's disease, anorexia, osteoarthritis, a central nervous system disorder and a peripheral nervous system disorder. The present sequence is the human lysosomal lipase #1.		
XX	SQ	Sequence 398 AA;	Query Match 88.6%; Score 1991; DB 23; Length 398; Best Local Similarity 100.0%; Pred. No. 9e-194; Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	50	SEIQHQGYCPEEYEVATEDCYLSVNRIPRGLYQPKKTGSRPVYLQHSLVGGASNWIS 109		Query Match 88.6%; Score 1991; DB 23; Length 398; Best Local Similarity 100.0%; Pred. No. 9e-194; Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	25	SEIQHQGYCPEEYEVATEDCYLSVNRIPRGLYQPKKTGSRPVYLQHSLVGGASNWIS 84		Qy 50 SEIQHQGYCPEEYEVATEDCYLSVNRIPRGLYQPKKTGSRPVYLQHSLVGGASNWIS 109
Qy	110	NLPNNSLGFILADAGFDWGNRSNAWSRKHKTLSIDQDEFWASYDEMAREFDLPAVIN 169		Db 25 SEIQHQGYCPEEYEVATEDCYLSVNRIPRGLYQPKKTGSRPVYLQHSLVGGASNWIS 84
Db	85	NLPNNSLGFILADAGFDWGNRSNAWSRKHKTLSIDQDEFWASYDEMAREFDLPAVIN 144		Qy 110 NLPNNSLGFILADAGFDWGNRSNAWSRKHKTLSIDQDEFWASYDEMAREFDLPAVIN 169
Qy	170	FILQTKQEKKYYGQSGTTMGMFIAFSTMPLEAKIKMYFALAPATVKAHKSPGTKFL 229		Db 85 NLPNNSLGFILADAGFDWGNRSNAWSRKHKTLSIDQDEFWASYDEMAREFDLPAVIN 144
Db	145	FILQTKQEKKYYGQSGTTMGMFIAFSTMPLEAKIKMYFALAPATVKAHKSPGTKFL 204		Qy 170 FILQTKQEKKYYGQSGTTMGMFIAFSTMPLEAKIKMYFALAPATVKAHKSPGTKFL 229
Qy	230	LLPDAMIKGLFGKKFELYQTRFLRQVLYLGQVYLDQICNSNIMLLGGFTNNNMSRA 289		Db 145 FILQTKQEKKYYGQSGTTMGMFIAFSTMPLEAKIKMYFALAPATVKAHKSPGTKFL 204
Db	205	LLPDAMIKGLFGKKFELYQTRFLRQVLYLGQVYLDQICNSNIMLLGGFTNNNMSRA 264		Qy 230 LLPDAMIKGLFGKKFELYQTRFLRQVLYLGQVYLDQICNSNIMLLGGFTNNNMSRA 289
Qy	290	SVAHTLAGTSVQNLHWSOAVNSSELRAFDWGSSETKMLEKCNQOPTPVRVRDMVPT 349		Db 205 LLPDAMIKGLFGKKFELYQTRFLRQVLYLGQVYLDQICNSNIMLLGGFTNNNMSRA 264
Db	265	SVAHTLAGTSVQNLHWSOAVNSSELRAFDWGSSETKMLEKCNQOPTPVRVRDMVPT 324		Qy 290 SVAHTLAGTSVQNLHWSOAVNSSELRAFDWGSSETKMLEKCNQOPTPVRVRDMVPT 349
Qy	350	AMWTGQDWLSNPEDVKMLLSEVTNLHKNIPENAHVDFIWGLDAPHMYNEIITHLMOQ 409		Db 265 SVAHTLAGTSVQNLHWSOAVNSSELRAFDWGSSETKMLEKCNQOPTPVRVRDMVPT 324
Db	325	AMWTGQDWLSNPEDVKMLLSEVTNLHKNIPENAHVDFIWGLDAPHMYNEIITHLMOQ 384		Qy 350 AMWTGQDWLSNPEDVKMLLSEVTNLHKNIPENAHVDFIWGLDAPHMYNEIITHLMOQ 409
Qy	410	ETENLISQGRCEAVL 423	Query Match 68.4%; Score 1536.5; DB 23; Length 371; Best Local Similarity 80.9%; Pred. No. 1.5e-17; Mismatches 17; Indels 22; Gaps 2;	Db 325 AMWTGQDWLSNPEDVKMLLSEVTNLHKNIPENAHVDFIWGLDAPHMYNEIITHLMOQ 384
Db	385	ETENLISQGRCEAVL 398	Qy 410 ETENLISQGRCEAVL 423	
RESULT 5	AAU99165	AAU99165 standard; Protein; 371 AA.	Db 385 ETENLISQGRCEAVL 398	
XX	AC	AAU99165;		
XX	DT	24-SEP-2002 (first entry)		

CC Alzheimer's disease, senile dementia, Huntington's disease, amyotrophic lateral sclerosis, Parkinson's, Gilles de la Tourette's syndrome, CC neuropsychiatric disorders such as hypertension and sleep disorders, CC anxiety, and bipolar affective disorder. The present sequence is a CC sequence used in a sequence homology alignment with the TANGO/INTERCEPT XX sequences of the present invention.

Sequence 399 AA;

Query Match 57.4%; Score 1289; DB 22; Length 399;

Best Local Similarity 63.5%; Pred. No. 2.7e-122; Conservative 55; Mismatches 80; Indels 0; Gaps 0;

Db 40 AVDPFAFMNISEIIQHGYCPEEYEVATEDGYILSVNRPVIRPGLYQPKKTGSRPVYLLQHG 99

Db 28 AVDPETNMVNEYSEIIISYWGFSSEEVLYETEGYLQCLNRPGRKHSKDGPVKPVFLQHG 87

Qy 100 LYGGASNWISNLPNNSLGFILADAGFDVWGNNSRGNASWRKHKTLSDQDEFWAFSYDEM 159

Db 88 LLADDSNWKVNTNLANSLSLGFILADAGFDVWGNNSRONTWSRKHKTLSVSQDEFWAFSYDEM 147

Qy 160 ARFDLPAVINFLILQTKGQEKIYVGSQGTTMGFIAFSTMPLEAKIKMFALAPATVK 219

Db 148 AKYDLPASINFILNKTGQEQVYVHSQGTTIGFTAFSOPLEAKRIMFALGVASVA 207

Qy 220 HAKSPGTKFLLPDAMIKGLEKFLKFLYQTRFLRQLVYLGQVILDQICSNIMLLGGF 279

Db 208 FCTSPMAKLRGPDLIKLDFGKFLPQSAFLKWLGTCTVHLKELGNLCFLCGF 267

Qy 280 NTNNNMMSRASVYAAHTLAGTSVONLHWSOAVNSGELRAFDWGSSETKNEKCNQPTPVR 339

Db 268 NERNLNMSRVDVYTHSPACTSVQNLHWSQAVKQFKQAFDWGSSAKNYFHYNOSYPP 327

Qy 340 YRVRDMTVPAWMTGQDMLSEVTLIYHKNIPAEAHVDFIWGLDAPHRM 399

Db 328 YNVRKOMLVPFAWSSGHDWLADYDVNILLQITNLVHESIPENELDFIWGLDAPWRL 387

Qy 400 YNEIHLMLQQ 409

Db 388 YNKITNLMRK 397

RESULT 8
ID AAO18227 standard; Protein: 392 AA.
XX AAO18227;
XX DT 18-SEP-2002 (first entry)

DE Human lysosomal acid lipase related protein.

XX Human; lysosomal acid lipase; chromosome 10; lipemeric; Wolman disease; XX cholestryler ester storage disease.
XX Homo sapiens.
XX US6387680-B1.
XX (PEKE) PE CORP NY.
XX 14-MAY-2002.
XX 29-MAR-2001; 2001US-0820001.
XX PR 29-MAR-2001; 2001US-0820001.

XX PN XX
XX PA XX
XX PD XX
XX PI XX
XX DR XX
PT PT

Isolated nucleic acids encoding a lysosomal acid lipase protein useful

for the prevention, diagnosis and treatment of severe infantile-onset Wolman disease and late-onset cholestryler ester storage disease - Disclosure: Column 57-60; 68pp; English.
XX
CC The present invention provides the protein, coding and genomic sequences of a human lysosomal acid lipase. The sequences can be used in the identification of modulators of lipase activity in cells and tissues that express the lipase, particularly the severe infantile-onset Wolman disease and the milder late-onset cholestryler ester storage disease (CESD), which are caused by mutations in different parts of the lysosomal acid lipase (LIP) gene. The present sequence is a protein shown in the exemplification of the invention.

Sequence 392 AA;

Query Match 57.1%; Score 1282; DB 23; Length 392;

Best Local Similarity 63.8%; Pred. No. 1.4e-121; Mismatches 53; Indels 0; Gaps 0;

Db 40 AVDPFAFMNISEIIQHGYCPEEYEVATEDGYILSVNRPVIRPGLYQPKKTGSRPVYLLQHG 99

Db 26 AVDPETNMVNEYSEIIISYWGFSSEEVLYETEGYLQCLNRPGRKHSKDGPVKPVFLQHG 85

Qy 100 LYGGASNWISNLPNNSLGFILADAGFDVWGNNSRGNASWRKHKTLSDQDEFWAFSYDEM 159

Db 86 1LADSSNWTNLANSLSLGFILADAGFDVWGNNSRONTWSRKHKTLSVSQDEFWAFSYDEM 145

Qy 160 ARFDLPAVINFLILQTKGQEKIYVGSQGTTMGFIAFSTMPLEAKIKMFALAPATVK 219

Db 146 AKYDLPASINFILNKTGQEQVYVHSQGTTIGFTAFSOPLEAKRIMFALGVASVA 205

Qy 220 HAKSPGTKFLLPDAMIKGLEKFLKFLYQTRFLRQLVYLGQVILDQICSNIMLLGGF 279

Db 206 FCTSPMAKLRGPDLIKLDFGKFLPQSAFLKWLGTCTVHLKELGNLCFLCGF 267

Qy 280 NTNNNMMSRASVYAAHTLAGTSVONLHWSOAVNSGELRAFDWGSSETKNEKCNQPTPVR 339

Db 266 NERNLNMSRVDVYTHSPACTSVQNLHWSQAVKQFKQAFDWGSSAKNYFHYNOSYPP 325

Qy 340 YRVRDMTVPAWMTGQDMLSEVTLIYHKNIPAEAHVDFIWGLDAPHRM 399

Db 328 YNVRKOMLVPFAWSSGHDWLADYDVNILLQITNLVHESIPENELDFIWGLDAPWRL 387

Qy 400 YNEIHLMLQQ 409

Db 386 YNKKIHL 392

RESULT 9
ID AAU30498 standard; Protein: 449 AA.

XX AAU30498;
XX AC AAU30498;

XX DT 18-DEC-2001 (first entry)

XX DE Novel human secreted protein #989.

XX Human; vaccination; gene therapy; nutritional supplement;

XX system cell proliferation; hematopoiesis; nerve tissue regeneration; XX immune suppression; immune stimulation; anti-inflammatory; leukaemia.

XX OS Homo sapiens.

XX PR WO200179449-A2.

XX PD 25-OCT-2001.

XX PR 16-APR-2001; 2001WO-US508656.

XX PR 26-JAN-2001; 2001US-0770160.

DE	RGL precursor.
XX	Rabbit gastric lipase; RGL; PRGLN2.1; fat; bioconversion;
KW	hydrolysis; transesterification.
KW	
XX	
OS	Oryctozeugus cuniculus.
XX	
Key	Location/Qualifiers
PH	23...398
FT	/note= "claim 1; page 10-11"
FT	
PN	EP542625-A.
PN	
XX	19-MAY-1993.
PD	
XX	92EP-0403055.
PF	
XX	12-NOV-1992;
PF	
XX	13-NOV-1991;
PR	
XX	91FR-0013948.
PA	
XX	(IJOU) INST RECH JOUVEINAL.
PI	Benicourt C, Blanchard C, Junien J;
XX	
WPI	1993-161080/20.
DR	
DR	N/PSDB; AAQ42310.
XX	
PT	Rabbit gastric lipase, its precursor and their DNA - useful
PT	treating conditions linked to gastric lipase deficiency, a
PT	mucoviscidosis and pancreatic exocrine insufficiency
XX	
PS	Claim 1; Fig 7; 31pp; French.

RESULT 11		Db	181 PIATVKHAKSITGKFLPDMIKGLFGKKFLYQTRFLRQ	221
ID AAB66068	Standard; Protein: 221 AA.			
AC AAB66068;				
XX				
DT 30-MAR-2001 (first entry)				
XX				
DE Human TANGO 294 extracellular domain.				
XX				
KW TANGO protein; INTERCEPT protein; neurological disorder; focal brain disorder; bipolar affective disorder; central nervous system; global-diffuse cerebral disorder; cerebrovascular; Alzheimer's disease; senile dementia; Huntington's disease; amyotrophic lateral sclerosis; Parkinson's; Gilles de la Tourette's syndrome; hypertension; sleep; neuro-psychiatric; psychoactive substance use; anxiety.				
XX				
OS Homo sapiens.				
XX				
PN WO2000077239-A2.				
XX				
PD 21-DEC-2000.				
XX				
PF 24-MAY-2000; 20000W0-US14858.				
XX				
PR 14-JUN-1999; 99US-03333159.				
XX				
PA (MILL-) MILLENNIUM PHARM INC.				
XX				
PI McCarthy SA, Fraser CC, Sharp JD, Barnes TM;				
XX				
DR WPI: 2001-032313/04.				
XX				
PT TANGO and INTERCEPT nucleic acids, proteins, and antibodies, useful for screening assays, and diagnostic assays and for the treatment of neurological diseases such as Alzheimer's, Parkinson's and Huntington's disease.				
XX				
PS Claim 8; Page 326; 359pp; English.				
XX				
CC The present invention relates to TANGO or INTERCEPT proteins and coding sequences (see AAF45121-45136 and AAF45138-45139 and AAB66031-66057, AAB66064-66083 and AAB66085). The TANGO/INTERCEPT Proteins and coding sequences are useful for the treatment of neurological disorders such as brain disorders, global-diffuse cerebral disorders and other CNS disorders, CNS-related disorders, focal neurologic and cerebrovascular disorders. The CNS disorders include Alzheimer's disease, senile dementia, Huntington's disease, amyotrophic lateral sclerosis, Parkinson's disease, Gilles de la Tourette's syndrome, neuro-psychiatric disorders such as hypertension and sleep disorders, neuro-psychiatric disorders, psychoactive substance use disorders, anxiety, and bipolar affective disorder.				
XX				
SQ Sequence 221 AA;				
Query Match 51.8%; Score 1165; DB 22; Length 221;				
Best Local Similarity 100.0%; Pred. No. 4.6e-110;				
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
XX				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 93				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 60				
Query Match 51.8%; Score 1165; DB 22; Length 221;				
Best Local Similarity 100.0%; Pred. No. 4.6e-110;				
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
XX				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 93				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 60				
Query Match 51.8%; Score 1165; DB 22; Length 221;				
Best Local Similarity 100.0%; Pred. No. 4.6e-110;				
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
XX				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 93				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 60				
Query Match 51.8%; Score 1165; DB 22; Length 221;				
Best Local Similarity 100.0%; Pred. No. 4.6e-110;				
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
XX				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 93				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 60				
Query Match 51.8%; Score 1165; DB 22; Length 221;				
Best Local Similarity 100.0%; Pred. No. 4.6e-110;				
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
XX				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 93				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 60				
Query Match 51.8%; Score 1165; DB 22; Length 221;				
Best Local Similarity 100.0%; Pred. No. 4.6e-110;				
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
XX				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 93				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 60				
Query Match 51.8%; Score 1165; DB 22; Length 221;				
Best Local Similarity 100.0%; Pred. No. 4.6e-110;				
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
XX				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 93				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 60				
Query Match 51.8%; Score 1165; DB 22; Length 221;				
Best Local Similarity 100.0%; Pred. No. 4.6e-110;				
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
XX				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 93				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 60				
Query Match 51.8%; Score 1165; DB 22; Length 221;				
Best Local Similarity 100.0%; Pred. No. 4.6e-110;				
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
XX				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 93				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 60				
Query Match 51.8%; Score 1165; DB 22; Length 221;				
Best Local Similarity 100.0%; Pred. No. 4.6e-110;				
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
XX				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 93				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 60				
Query Match 51.8%; Score 1165; DB 22; Length 221;				
Best Local Similarity 100.0%; Pred. No. 4.6e-110;				
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
XX				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 93				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 60				
Query Match 51.8%; Score 1165; DB 22; Length 221;				
Best Local Similarity 100.0%; Pred. No. 4.6e-110;				
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
XX				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 93				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 60				
Query Match 51.8%; Score 1165; DB 22; Length 221;				
Best Local Similarity 100.0%; Pred. No. 4.6e-110;				
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
XX				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 93				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 60				
Query Match 51.8%; Score 1165; DB 22; Length 221;				
Best Local Similarity 100.0%; Pred. No. 4.6e-110;				
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
XX				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 93				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 60				
Query Match 51.8%; Score 1165; DB 22; Length 221;				
Best Local Similarity 100.0%; Pred. No. 4.6e-110;				
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
XX				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 93				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 60				
Query Match 51.8%; Score 1165; DB 22; Length 221;				
Best Local Similarity 100.0%; Pred. No. 4.6e-110;				
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
XX				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 93				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 60				
Query Match 51.8%; Score 1165; DB 22; Length 221;				
Best Local Similarity 100.0%; Pred. No. 4.6e-110;				
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
XX				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 93				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 60				
Query Match 51.8%; Score 1165; DB 22; Length 221;				
Best Local Similarity 100.0%; Pred. No. 4.6e-110;				
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
XX				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 93				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 60				
Query Match 51.8%; Score 1165; DB 22; Length 221;				
Best Local Similarity 100.0%; Pred. No. 4.6e-110;				
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
XX				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 93				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 60				
Query Match 51.8%; Score 1165; DB 22; Length 221;				
Best Local Similarity 100.0%; Pred. No. 4.6e-110;				
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
XX				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 93				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 60				
Query Match 51.8%; Score 1165; DB 22; Length 221;				
Best Local Similarity 100.0%; Pred. No. 4.6e-110;				
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
XX				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 93				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 60				
Query Match 51.8%; Score 1165; DB 22; Length 221;				
Best Local Similarity 100.0%; Pred. No. 4.6e-110;				
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
XX				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 93				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 60				
Query Match 51.8%; Score 1165; DB 22; Length 221;				
Best Local Similarity 100.0%; Pred. No. 4.6e-110;				
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
XX				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 93				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 60				
Query Match 51.8%; Score 1165; DB 22; Length 221;				
Best Local Similarity 100.0%; Pred. No. 4.6e-110;				
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
XX				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 93				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 60				
Query Match 51.8%; Score 1165; DB 22; Length 221;				
Best Local Similarity 100.0%; Pred. No. 4.6e-110;				
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
XX				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 93				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 60				
Query Match 51.8%; Score 1165; DB 22; Length 221;				
Best Local Similarity 100.0%; Pred. No. 4.6e-110;				
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
XX				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 93				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 60				
Query Match 51.8%; Score 1165; DB 22; Length 221;				
Best Local Similarity 100.0%; Pred. No. 4.6e-110;				
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
XX				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 93				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 60				
Query Match 51.8%; Score 1165; DB 22; Length 221;				
Best Local Similarity 100.0%; Pred. No. 4.6e-110;				
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
XX				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 93				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 60				
Query Match 51.8%; Score 1165; DB 22; Length 221;				
Best Local Similarity 100.0%; Pred. No. 4.6e-110;				
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
XX				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 93				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 60				
Query Match 51.8%; Score 1165; DB 22; Length 221;				
Best Local Similarity 100.0%; Pred. No. 4.6e-110;				
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
XX				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 93				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 60				
Query Match 51.8%; Score 1165; DB 22; Length 221;				
Best Local Similarity 100.0%; Pred. No. 4.6e-110;				
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
XX				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 93				
Db 1 VHMPTKAVDPEAFMNISETIQQGKPEEEVATEDGYIISVNRIPRGLYQPKKTSRVPY 60				
Query Match 51.8%; Score 1165; DB 22; Length 221;				
Best Local Similarity 100.0%; Pred. No. 4.6e-110;	</			

PT preventing immune system disorders (e.g. Crohn's disease), neurological disorders (e.g. Parkinson's disease), or cell proliferative disorders (e.g. cancers) -
 PT XX
 PS Claim 48; Page 111-112; 122pp; English.
 CC The present invention relates to the isolation of human lipid metabolism enzymes (LMM) designated LMM-1 to LMM-6, and the polynucleotide sequences encoding them. The LMM polypeptides, CC polynucleotides, agonists and antagonists are useful for diagnosing, treating or preventing disorders associated with aberrant expression of LMM, particularly immune system disorders (e.g. acquired immunodeficiency syndrome (AIDS), thymic hypoplasia, anaemia, asthma or Crohn's disease), neurological disorders (e.g. epilepsy, Huntington's disease, dementia or Parkinson's disease), developmental disorders (e.g. Down's syndrome) or cell proliferative disorders (e.g. cancers including adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma or sarcoma). The present sequence represents human LMM-4.
 XX Sequence 399 AA;

Query Match 50.9%; Score 1143; DB 23; Length 399;
 Best Local Similarity 54.2%; Pred. No. 2e-107;
 Matches 213; Conservative 71; Mismatches 101; Indels 8; Gaps 2;
 Qy 18 WLLILYA-YMFQRTVNSVHMPTKAVDPEAFWNISIIOHQYCPCEYEVATEDGIVLSVN 76
 Db 10 WMLLGSMSYGDKGKGNN-----ANPEANNNISQISIWSYKPYEYDVTKDGYTIGY 62
 SQ sequence 399 AA;

Query Match 77 RIPRGLVYQPKKTGSPRPVVLQHVGASWNSLPNNNSGPILADAGFDVWGNNSRGNNA 136
 Best Local Similarity 56.5%; Pred. No. 2.6e-107;
 Matches 210; Conservative 67; Mismatches 90; Indels 5; Gaps 3;
 Qy 137 WSRKHTLSSIDQDEFWAFSYDEMAFEDLPAYINFVLOKTOGKQKIIYVGYSGQTMGTFIAF 196
 Db 123 WSRKHLKLSPSPPEWAFSDEMAKDLPATINFVLEKTOGKRLVYVGHSGOTTIAFIAF 182
 Qy 197 STMPELAQKIMYFALAPIATVKAHSKSPGTKEFLLPDDMMIGLFGKEFYOTRFRLQLV 256
 Db 183 STMPELAQKIMYFALAPIATVKAHSKSPGTKEFLLPDDMMIGLFGKEFYOTRFRLQLV 242
 Qy 257 IYLGQVILQDQCSNIMLGGFTNMMMSRASVYAAHTLAGTSVONILHNSQAVNSGE 316
 Db 243 TKVCRNRLFRRCISNLFQTLSSQFDQNLNSMSRLDYZLSHNPAGTSVQNMHLWAQAVNSGQ 302
 Qy 317 LRAFDNGSETKNLEKCNQPTPVRYRVDMTVPTAMTQGDWNLSPNPDVKMULSEYTNLI 376
 Db 303 LQAFDNGSDQNMHMFIQLTPLYNTKMEVTAIWNGQDIVADPVDENILPQIANLI 362
 Qy 377 YHKNIPPEWAHYDFWIDPHAPNEETIHLMOQ 409
 Db 363 YKLIPHINHYDFYLGDAQPEQYQDLTILMEE 395

RESULT 15
 AAR56810;
 XX
 ID AAR56870 standard; Protein; 379 AA.
 DE Canine gastric lipase.
 XX
 KW Canine gastric lipase; CGL; dog; fat; mucoviscidosis; enzyme;
 KW bioconversion; exocrine pancreatic insufficiency.
 XX
 OS Canis familiaris.
 PN W09413816-A.
 XX
 DT 20-FEB-1995 (first entry)
 XX
 DE Canine gastric lipase.

PF 16-DEC-1993; 93WO-FR01260.
 PR 16-DEC-1992; 92FR-0015201.
 XX
 PA (LJOU) INST RECH JOUVEINAL.
 PI Benicourt C, Blanchard C, Junien J;
 XX
 WPI; 1994-217896/26.
 DR N-PSDB; AAQCB838E.
 XX recombinant canine gastric lipase and nucleic acid encoding it -
 PR are used for improving absorption of ingested fat, treating
 PR mucoviscidosis etc. and in enzymatic bio-conversions
 XX
 PS Claim 13; Fig 9A; 52pp; French.
 XX
 CC The sequence given below is the sequence of figure 9A, altered
 CC according to the amendments described on page 2 of the appended
 CC letter.
 CC CGL is used to improve absorption of ingested fat, in healthy and
 CC sick patients (e.g. having altered levels of gastric lipase); to
 CC treat conditions associated with insufficiency (or lack) of lipases,
 CC esp. mucoviscidosis or exocrine pancreatic insufficiency and partic.
 CC where immobilised, for biotransformations, e.g. hydrolysis or
 CC transesterification (other mammalian gastric lipases, or derivs.,
 CC can be used in this application).
 XX
 SQ sequence 379 AA;

Query Match 50.8%; Score 1141.5; DB 15; Length 379;
 Best Local Similarity 56.5%; Pred. No. 2.6e-107;
 Matches 210; Conservative 67; Mismatches 90; Indels 5; Gaps 3;
 Qy 37 PIKAVDPEAFMNTSEIIOHQGIPCEEEVATEADGYIILSVNRPGLVYQPKTGSPRVYLL 96
 Db 7 PT --NPEVNTNISOMTGYGPAEEYEVVTDGYIIGIDRIPYGRKSENIGRPPAFL 63
 Qy 97 QHGLVGASNTNSNLPNNSLAFGLADAGFDVWGNNSRGNNAERKHTLSSIDQDEFASY 156
 Db 64 QHQLLSATNTNISNLNPNNSLAFLADAGFDVWGNNSRGNNTWARRNLYYSPDSEVFNAFSF 123
 Qy 157 DEMARFDLPATVINFILQTKQEMIYVGYSGQTMGTFIAFIMPMLAQKIMYFALAPIA 216
 Db 124 DEMAKYDLPATIDFILKTKGQDKLHYVGHSGQTIGFIAFSTNPKLAKRKTDFYALAPVA 183
 Qy 217 TVKHAQSPGTQFLPDMIGKFGKEFYOTRFRLQ-LVYILCGQVYLIDOCNSNMLL 275
 Db 184 TVXETELUNKLMLVPSFLKFLGFKNIF-YPHFFDQFLATEVCSSRETVLCSNLF1 242
 Qy 276 LGGFNTNMMMSRASVYAAHTLAGTSVONILHNSQAVNSGEYSGTML 335
 Db 243 ICGFDTMNLNMSRLDYZLSHNPAGTSVQNLHNSQAVSKGKQAFDNGSPVQNMHYHQS 302
 Qy 336 TPVYRVDMTVPTAMTQGDWNLSPNPDVKMULSEVNLTHKNPEWAHYDFWGLDA 395
 Db 303 MPYYNLTDMHYPIAVWNGNDLADPHDVLILSKPLNLYHCKIPPYNHDFIRAMDA 362
 Qy 396 PHMYNEITHLM 407
 Db 363 PQAVYNEIVSM 374

search completed: February 3, 2003, 13:48:54
 Job time : 41 secs

GenCore version 5.1.3					
Copyright (c) 1993 - 2003 Compugen Ltd.					
4 protein - protein search, using sw model					
run on:	February 3, 2003	13:50:05	Search time 13 Seconds		
			(without alignments)		
			636.579 Million cell updates/sec		
title:	US-09-333-159-47				
perfect score:	2247				
sequence:	1 MLETLSRQIVSHRMEMWLL.....	IHLMQQETNLSQLRCEAVL	423	
scoring table:	BLOSUM62				
searched:	Gapop 10.0	Gapext 0.5			
total number of hits satisfying chosen parameters:	122226	seqs, 20178551 residues			
minimum DB seq length:	0				
maximum DB seq length:	2000000000				
post-processing:	Minimum Match 0%				
	Maximum Match 100%				
	Listing first 45 summaries				
database:	Published Applications_AA: * /cgns_2_6/ptodata/2/pubpaa/US08_NEW_PUB..pep: * 2: /cgns_2_6/ptodata/2/pubpaa/US05_PCTUS_NEW_PUB..pep: * 3: /cgns_2_6/ptodata/2/pubpaa/US06_NEW_PUB..pep: * 4: /cgns_2_6/ptodata/2/pubpaa/US06_PUBCOMB..pep: * 5: /cgns_2_6/ptodata/2/pubpaa/US07_NEW_PUB..pep: * 6: /cgns_2_6/ptodata/2/pubpaa/US07_PUBCOMB..pep: * 7: /cgns_2_6/ptodata/2/pubpaa/PTCTS_PUBCOMB..pep: * 8: /cgns_2_6/ptodata/2/pubpaa/US08_PUBCOMB..pep: * 9: /cgns_2_6/ptodata/2/pubpaa/US09_NEW_PUB..pep: * 10: /cgns_2_6/ptodata/2/pubpaa/US09_PUBCOMB..pep: * 11: /cgns_2_6/ptodata/2/pubpaa/US10_NEW_PUB..pep: * 12: /cgns_2_6/ptodata/2/pubpaa/US10_PUBCOMB..pep: * 13: /cgns_2_6/ptodata/2/pubpaa/US60_NEW_PUB..pep: * 14: /cgns_2_6/ptodata/2/pubpaa/US60_PUBCOMB..pep: *				
pred. No.	is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
SUMMARIES					
result No.	Score	Query Match	Length	DB ID	Description
1	2247	100.0	423	9 US-10-042-411-47	Sequence 47, Ap
2	2174	96.8	409	10 US-09-835-396A-21	Sequence 21, A
3	2016	92.4	390	9 US-10-042-411-49	Sequence 49, Ap
4	1991	88.6	374	10 US-09-811-325-4	Sequence 4, Ap
5	1991	88.6	398	10 US-09-811-325-2	Sequence 2, Ap
6	1289	57.4	399	9 US-10-042-411-41	Sequence 41, Ap
7	1282	57.1	392	12 US-10-003-302-4	Sequence 4, Ap
8	1165	51.8	221	9 US-10-042-411-50	Sequence 50, Ap
9	1119	49.8	398	9 US-10-042-411-75	Sequence 75, Ap
10	1090	48.5	398	9 US-10-056-744B-2	Sequence 2, Ap
11	1031	45.9	395	12 US-10-003-302-2	Sequence 2, Ap
12	783	34.8	144	9 US-10-042-411-52	Sequence 52, Ap
13	400	34.8	127	9 US-10-056-744B-5	Sequence 5, Ap
14	171	7.6	33	9 US-10-042-411-48	Sequence 48, Ap
15	128	5.7	25	9 US-10-042-411-51	Sequence 51, Ap
16	1095	4.9	305	10 US-09-815-342-12337	Sequence 12337, Ap
17	103	4.6	222	10 US-09-815-242-5276	Sequence 5276, Ap
18	102	4.5	346	9 US-10-057-885-34	Sequence 34, Ap
19	102	4.5	346	9 US-09-803-310-34	Sequence 34, Ap

20	99	9	US-09-738-6262-6025-	Sequence 6025, Ap
21	96.5	9	US-10-080-644-4	Sequence 4, Appl 1
22	96.5	9	US-10-035-201-3	Sequence 3, Appl 1
23	95.5	9	US-10-005-1835-1-189	Sequence 189, Ap
24	93	9	US-09-738-6262-4721	Sequence 4721, Ap
25	92	4.1	US-09-738-6262-4720-8	Sequence 10278, Ap
26	92	4.1	US-09-615-242-13880	Sequence 13880, Ap
27	91	4.0	US-09-615-242-13880	Sequence 6, Appl 1
28	89	4.0	US-09-950-3488-6	Sequence 2, Appl 1
29	87.5	3.9	US-09-996-578-2	Sequence 7, Appl 1
30	86.5	3.8	US-10-080-644-7	Sequence 4289, Ap
31	86.5	3.8	US-09-738-6262-4289	Sequence 6, Appl 1
32	85	3.8	US-09-839-849-6	Sequence 2, Appl 1
33	84.5	3.8	US-10-073-737A-2	Sequence 40, Appl 1
34	84.5	3.8	US-10-027-805-4	Sequence 40, Appl 1
35	84	3.7	US-09-903-410-40	Sequence 1, Appl 1
36	82.5	3.7	US-09-967-645-1	Sequence 3832, Ap
37	82.5	3.7	US-09-918-543-2	Sequence 2, Appl 1
38	82.5	3.7	US-09-795-211-1	Sequence 1, Appl 1
39	82.5	3.7	US-09-669-864-1	Sequence 7, Appl 1
40	82.5	3.7	US-09-659-864-7	Sequence 2, Appl 1
41	82.5	3.7	US-09-854-346-2	Sequence 1, Appl 1
42	82.5	3.7	US-09-902-1188A-1	Sequence 30, Appl 1
43	82	3.6	US-10-051-643-3-0	Sequence 30, Appl 1
44	82	3.6	US-09-880-505-3-0	Sequence 13, Appl 1
45	81.5	3.6	US-09-918-543-1-13	Sequence 13, Appl 1

ALIGNMENTS

SUMMARIES							
Result No.	Score	Query Match	Length	DB ID	8	Query Match	Length
1	2247	100.0	423	9	US-10-042-411-47	Sequence 47, AP	
2	2174	96.8	409	10	US-09-835-596-A-21	Sequence 21, A	
3	2016	92.4	390	9	US-10-042-411-49	Sequence 49, AP	
4	1991	88.6	374	10	US-09-811-025-4	Sequence 4, AP	
5	1991	88.6	398	10	US-09-811-025-2	Sequence 2, AP	
6	1289	57.4	399	9	US-10-042-411-41	Sequence 41, AP	
7	1282	57.1	392	12	US-10-003-002-4	Sequence 4, AP	
8	1165	51.8	221	9	US-10-042-411-50	Sequence 50, AP	
9	1119	49.8	398	9	US-10-042-411-75	Sequence 75, AP	
10	1000	48.5	398	9	US-10-056-74AB-2	Sequence 2, AP	
11	1031	45.9	395	12	US-10-003-002-2	Sequence 2, AP	
12	783	34.8	144	9	US-10-042-411-52	Sequence 52, AP	
13	400	17.8	127	9	US-10-056-74AB-5	Sequence 5, AP	
14	171	7.6	33	9	US-10-042-411-48	Sequence 48, AP	
15	128	5.7	25	9	US-10-042-411-51	Sequence 51, AP	
16	109.5	4.9	305	10	US-09-815-042-12337	Sequence 12337, AP	
17	103	4.6	222	10	US-09-815-242-5276	Sequence 5276, AP	
18	102	4.5	346	9	US-10-057-805-34	Sequence 34, AP	
19	102	4.5	346	10	US-09-903-010-34	Sequence 34, AP	

Qy	181 YYVGYSQCTTMGFIASFSTMPLEAQKIKMYFALAPIATVKHAKSPGTKFLLPDMMIKGFL 240	Qy	135 NAMSRKHTLSIDQDEFWAFSTDEMARFDLPAVINFLQKTOEKIYVYSGQTGMFI 194
Db	181 YYVGYSQCTTMGFIASFSTMPLEAQKIKMYFALAPIATVKHAKSPGTKFLLPDMMIKGFL 240	Db	121 NAMSRKHTLSIDQDEFWAFSTDEMARFDLPAVINFLQKTOEKIYVYSGQTGMFI 180
Qy	241 GKKEFLYOTRFLQVLVLYLCGVQVLDQICNSNMLLGGFTNTNNMRSASYAHTLAGT 300	Qy	195 AFSTMPLEAQKIKMYFALAPIATVKHAKSPGTKFLLPDMMIKGFLGKKEFLYOTRFLQ 254
Db	241 GKKEFLYOTRFLQVLVLYLCGVQVLDQICNSNMLLGGFTNTNNMRSASYAHTLAGT 300	Db	181 AFSTMPLEAQKIKMYFALAPIATVKHAKSPGTKFLLPDMMIKGFLGKKEFLYOTRFLQ 240
Qy	301 SVQNLIHWSQAVNSGELRAFDNGSETKLNLEKCNQPTPVYRVDMTYPTAMTGGDOWLS 360	Qy	255 LIVYLGCVVNDQCSNTMILLLGGFTNTNNMRSASYAHTLAGTSQNLIHWSQAVNS 314
Db	301 SVQNLIHWSQAVNSGELRAFDNGSETKLNLEKCNQPTPVYRVDMTYPTAMTGGDOWLS 360	Db	241 LIVYLGCVVNDQCSNTMILLLGGFTNTNNMRSASYAHTLAGTSQNLIHWSQAVNS 300
Qy	361 NPEDVNMLLSEVTNLIYHKNPEWAHYDFINGDAPHRMYNEIILHMQQEETNLSQGRCE 420	Qy	315 GEIRAFTDGSETEKNLEKCNQPTPVYRVDMTYPTAMTGGDOWLSNPEDVNMLLSEVTN 374
Db	361 NPEDVNMLLSEVTNLIYHKNPEWAHYDFINGDAPHRMYNEIILHMQQEETNLSQGRCE 420	Db	301 GEIRAFTDGSETEKNLEKCNQPTPVYRVDMTYPTAMTGGDOWLSNPEDVNMLLSEVTN 360
Qy	421 AVL 423	Qy	375 LIYHKNIPEWAHYDFINGDAPHRMYNEIILHMQQEETNLSQGRCEAVL 423
Db	421 AVL 423	Db	361 LIYHKNIPEWAHYDFINGDAPHRMYNEIILHMQQEETNLSQGRCEAVL 409
RESULT 2			
US-09-835-996A-21			
Sequence 21, Application US/09835996A			
; Patent No. US20020142953A1			
; GENERAL INFORMATION:			
; APPLICANT: Ballinger, Dennis			
; APPLICANT: Loeb, Debra			
; APPLICANT: Montgomery, Julie			
; APPLICANT: Tang, Y. Tom			
; APPLICANT: Zhou, Ping			
; APPLICANT: Goodrich, Ryle			
; APPLICANT: Liu, Chenghua			
; APPLICANT: Asundi, Vinod			
; APPLICANT: Zhao, Qing			
; APPLICANT: Wehrman, Tom			
; APPLICANT: Dumanac, Radoje			
; APPLICANT: Ren, Feiyan			
; APPLICANT: Qian, Xiaohong			
; APPLICANT: Wang, Dunrui			
; TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO LIPID METABOLISM			
; CURRENT APPLICATION NUMBER: US/09/835,996A			
; CURRENT FILING DATE: 2001-04-16			
; PRIOR APPLICATION NUMBER: US 09/714,936			
; PRIOR FILING DATE: 2000-04-14			
; PRIOR APPLICATION NUMBER: US 09/667,298			
; PRIOR FILING DATE: 2000-09-22			
; PRIOR FILING DATE: 2000-08-03			
; PRIOR APPLICATION NUMBER: US 09/598,042			
; PRIOR FILING DATE: 2000-06-20			
; NUMBER OF SEQ ID NOS: 45			
; SOFTWARE: PatentIn version 3.0			
; SEQ ID NO: 21			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-10-012-431-49			
Query Match 92.4%; Score 2076; DB 9; Length 390;			
Best Local Similarity 100.0%; Pred. No. 4 .9e-180; Mismatches 0; Indels 0; Gaps 0;			
; US-10-012-431-49			
RESULT 3			
US-10-042-431-49			
; Sequence 49, Application US/10042431			
; Publication No. US20020182675A1			
; GENERAL INFORMATION:			
; APPLICANT: MCCARTHY, Sean A			
; APPLICANT: BARNES, Thomas M			
; APPLICANT: FRASER, Christopher C			
; APPLICANT: SHARP, John D			
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC, THERAPEUTIC, AND OTHER USES			
; FILE PREFERENCE: 10147-6U2			
; CURRENT APPLICATION NUMBER: US/10/042431			
; CURRENT FILING DATE: 2001-10-25			
; PRIOR APPLICATION NUMBER: US 09/333,159			
; PRIOR FILING DATE: 1999-06-14			
; PRIOR APPLICATION NUMBER: US 09/578,063			
; PRIOR FILING DATE: 2000-05-24			
; NUMBER OF SEQ ID NOS: 79			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO: 49			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-10-012-431-49			
Query Match 92.4%; Score 2076; DB 9; Length 390;			
Best Local Similarity 100.0%; Pred. No. 4 .9e-180; Mismatches 0; Indels 0; Gaps 0;			
; US-10-012-431-49			
Query Match 92.4%; Score 2076; DB 9; Length 390;			
Best Local Similarity 100.0%; Pred. No. 4 .9e-180; Mismatches 0; Indels 0; Gaps 0;			
; US-10-012-431-49			
Query Match 92.4%; Score 2076; DB 9; Length 390;			
Best Local Similarity 100.0%; Pred. No. 4 .9e-180; Mismatches 0; Indels 0; Gaps 0;			
; US-10-012-431-49			
Query Match 92.4%; Score 2076; DB 9; Length 390;			
Best Local Similarity 100.0%; Pred. No. 4 .9e-180; Mismatches 0; Indels 0; Gaps 0;			
; US-10-012-431-49			
Query Match 92.4%; Score 2076; DB 9; Length 390;			
Best Local Similarity 100.0%; Pred. No. 4 .9e-180; Mismatches 0; Indels 0; Gaps 0;			
; US-10-012-431-49			
Query Match 92.4%; Score 2076; DB 9; Length 390;			
Best Local Similarity 100.0%; Pred. No. 4 .9e-180; Mismatches 0; Indels 0; Gaps 0;			
; US-10-012-431-49			
Query Match 92.4%; Score 2076; DB 9; Length 390;			
Best Local Similarity 100.0%; Pred. No. 4 .9e-180; Mismatches 0; Indels 0; Gaps 0;			
; US-10-012-431-49			
Query Match 92.4%; Score 2076; DB 9; Length 390;			
Best Local Similarity 100.0%; Pred. No. 4 .9e-180; Mismatches 0; Indels 0; Gaps 0;			
; US-10-012-431-49			
Query Match 92.4%; Score 2076; DB 9; Length 390;			
Best Local Similarity 100.0%; Pred. No. 4 .9e-180; Mismatches 0; Indels 0; Gaps 0;			
; US-10-012-431-49			
Query Match 92.4%; Score 2076; DB 9; Length 390;			
Best Local Similarity 100.0%; Pred. No. 4 .9e-180; Mismatches 0; Indels 0; Gaps 0;			
; US-10-012-431-49			
Query Match 92.4%; Score 2076; DB 9; Length 390;			
Best Local Similarity 100.0%; Pred. No. 4 .9e-180; Mismatches 0; Indels 0; Gaps 0;			
; US-10-012-431-49			
Query Match 92.4%; Score 2076; DB 9; Length 390;			
Best Local Similarity 100.0%; Pred. No. 4 .9e-180; Mismatches 0; Indels 0; Gaps 0;			
; US-10-012-431-49			
Query Match 92.4%; Score 2076; DB 9; Length 390;			
Best Local Similarity 100.0%; Pred. No. 4 .9e-180; Mismatches 0; Indels 0; Gaps 0;			
; US-10-012-431-49			
Query Match 92.4%; Score 2076; DB 9; Length 390;			
Best Local Similarity 100.0%; Pred. No. 4 .9e-180; Mismatches 0; Indels 0; Gaps 0;			
; US-10-012-431-49			
Query Match 92.4%; Score 2076; DB 9; Length 390;			
Best Local Similarity 100.0%; Pred. No. 4 .9e-180; Mismatches 0; Indels 0; Gaps 0;			
; US-10-012-431-49			
Query Match 92.4%; Score 2076; DB 9; Length 390;			
Best Local Similarity 100.0%; Pred. No. 4 .9e-180; Mismatches 0; Indels 0; Gaps 0;			
; US-10-012-431-49			
Query Match 92.4%; Score 2076; DB 9; Length 390;			
Best Local Similarity 100.0%; Pred. No. 4 .9e-180; Mismatches 0; Indels 0; Gaps 0;			
; US-10-012-431-49			
Query Match 92.4%; Score 2076; DB 9; Length 390;			
Best Local Similarity 100.0%; Pred. No. 4 .9e-180; Mismatches 0; Indels 0; Gaps 0;			
; US-10-012-431-49			
Query Match 92.4%; Score 2076; DB 9; Length 390;			
Best Local Similarity 100.0%; Pred. No. 4 .9e-180; Mismatches 0; Indels 0; Gaps 0;			
; US-10-012-431-49			
Query Match 92.4%; Score 2076; DB 9; Length 390;			
Best Local Similarity 100.0%; Pred. No. 4 .9e-180; Mismatches 0; Indels 0; Gaps 0;			
; US-10-012-431-49			
Query Match 92.4%; Score 2076; DB 9; Length 390;			
Best Local Similarity 100.0%; Pred. No. 4 .9e-180; Mismatches 0; Indels 0; Gaps 0;			
; US-10-012-431-49			
Query Match 92.4%; Score 2076; DB 9; Length 390;			
Best Local Similarity 100.0%; Pred. No. 4 .9e-180; Mismatches 0; Indels 0; Gaps 0;			
; US-10-012-431-49			
Query Match 92.4%; Score 2076; DB 9; Length 390;			
Best Local Similarity 100.0%; Pred. No. 4 .9e-180; Mismatches 0; Indels 0; Gaps 0;			
; US-10-012-431-49			
Query Match 92.4%; Score 2076; DB 9; Length 390;			
Best Local Similarity 100.0%; Pred. No. 4 .9e-180; Mismatches 0; Indels 0; Gaps 0;			
; US-10-012-431-49			
Query Match 92.4%; Score 2076; DB 9; Length 390;			
Best Local Similarity 100.0%; Pred. No. 4 .9e-180; Mismatches 0; Indels 0; Gaps 0;			
; US-10-012-431-49			
Query Match 92.4%; Score 2076; DB 9; Length 390;			
Best Local Similarity 100.0%; Pred. No. 4 .9e-180; Mismatches 0; Indels 0; Gaps 0;			
; US-10-012-431-49			
Query Match 92.4%; Score 2076; DB 9; Length 390;			
Best Local Similarity 100.0%; Pred. No. 4 .9e-180; Mismatches 0; Indels 0; Gaps 0;			
; US-10-012-431-49			
Query Match 92.4%; Score 2076; DB 9; Length 390;			
Best Local Similarity 100.0%; Pred. No. 4 .9e-180; Mismatches 0; Indels 0; Gaps 0;			
; US-10-012-431-49			
Query Match 92.4%; Score 2076; DB 9; Length 390;			
Best Local Similarity 100.0%; Pred. No. 4 .9e-180; Mismatches 0; Indels 0; Gaps 0;			
; US-10-012-431-49			
Query Match 92.4%; Score 2076; DB 9; Length 390;			
Best Local Similarity 100.0%; Pred. No. 4 .9e-180; Mismatches 0; Indels 0; Gaps 0;			
; US-10-012-431-49			
Query Match 92.4%; Score 2076; DB 9; Length 390;			
Best Local Similarity 100.0%; Pred. No. 4 .9e-180; Mismatches 0; Indels 0; Gaps 0;			
; US-10-012-431-49			
Query Match 92.4%; Score 2076; DB 9; Length 39			

		RESULT 4
Db	301	QPTVRYRVDMDTIVTAMTGGDQLNSNPDVKMLSEVNLIVKNIPEWAHVDFIWGL 360
Qy	394	DAPHMYNEIHLIQQEETNLSQGCEAVL 423
Db	361	DAPHMYNEIHLIQQEETNLSQGCEAVL 390
		Query Match
		Best Local Similarity
		Score 88.6%; Pred. No. 4.7e-180; Length 374;
		Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Qy	50	SEIIHQGYCEEYEVATEDGYIISVNIRPRLQVOKKTGSRPVVLLQHGLVGGASNWIS 109
Db	1	SEIIHQGYCEEYEVATEDGYIISVNIRPRLQVOKKTGSRPVVLLQHGLVGGASNWIS 60
Qy	110	NLPNNSLGFIILADGEFDWGNRSGNAWSRKHKTLSIDQDEFWAFSYDEMARFDLPAVIN 169
Db	61	NLPNNSLGFIILADGEFDWGNRSGNAWSRKHKTLSIDQDEFWAFSYDEMARFDLPAVIN 120
Qy	170	FILQTKQEKKIYGGSQGTMTGFAFSTMPLEAKTQKMYPALAPATVKHAKSPGTKFL 229
Db	121	FILQTKQEKKIYGGSQGTMTGFAFSTMPLEAKTQKMYPALAPATVKHAKSPGTKFL 180
Qy	230	LLPDMMIKGLFGKKFELYQTPLRQLVYIQLCQVILDQICSNIMLLGGENTNNMNSRA 289
Db	181	LLPDMMIKGLFGKKFELYQTPLRQLVYIQLCQVILDQICSNIMLLGGENTNNMNSRA 240
Qy	290	SVYAAHTLAGTSVQNLHWSAVNSGELRADPWSSETKNCNQPPVRYRVRDMVPT 349
Db	241	SVYAAHTLAGTSVQNLHWSAVNSGELRADPWSSETKNCNQPPVRYRVRDMVPT 300
Qy	350	AMWTGGDQLNSNPDVYKMLSEVNLIVKNIPEWAHVDFIWGLDAPHRYNEIHLIMQO 409
Db	301	AMWTGGDQLNSNPDVYKMLSEVNLIVKNIPEWAHVDFIWGLDAPHRYNEIHLIMQO 360
Qy	410	EETNLISQGRCEAVL 423
Db	361	EETNLISQGRCEAVL 374
		Query Match
		Best Local Similarity
		Score 88.6%; Pred. No. 4.7e-180; Length 374;
		Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Qy	50	SEIIHQGYCEEYEVATEDGYIISVNIRPRLQVOKKTGSRPVVLLQHGLVGGASNWIS 109
Db	1	SEIIHQGYCEEYEVATEDGYIISVNIRPRLQVOKKTGSRPVVLLQHGLVGGASNWIS 60
Qy	110	NLPNNSLGFIILADGEFDWGNRSGNAWSRKHKTLSIDQDEFWAFSYDEMARFDLPAVIN 169
Db	61	NLPNNSLGFIILADGEFDWGNRSGNAWSRKHKTLSIDQDEFWAFSYDEMARFDLPAVIN 120
Qy	170	FILQTKQEKKIYGGSQGTMTGFAFSTMPLEAKTQKMYPALAPATVKHAKSPGTKFL 229
Db	121	FILQTKQEKKIYGGSQGTMTGFAFSTMPLEAKTQKMYPALAPATVKHAKSPGTKFL 180
Qy	230	LLPDMMIKGLFGKKFELYQTPLRQLVYIQLCQVILDQICSNIMLLGGENTNNMNSRA 289
Db	181	LLPDMMIKGLFGKKFELYQTPLRQLVYIQLCQVILDQICSNIMLLGGENTNNMNSRA 240
Qy	290	SVYAAHTLAGTSVQNLHWSAVNSGELRADPWSSETKNCNQPPVRYRVRDMVPT 349
Db	241	SVYAAHTLAGTSVQNLHWSAVNSGELRADPWSSETKNCNQPPVRYRVRDMVPT 300
Qy	350	AMWTGGDQLNSNPDVYKMLSEVNLIVKNIPEWAHVDFIWGLDAPHRYNEIHLIMQO 409
Db	301	AMWTGGDQLNSNPDVYKMLSEVNLIVKNIPEWAHVDFIWGLDAPHRYNEIHLIMQO 360
Qy	410	EETNLISQGRCEAVL 423
Db	361	EETNLISQGRCEAVL 374
		RESULT 5
		US-09-811-825-2
		Sequence 2, Application US/09811825
		Patent No. US20020442971
		GENERAL INFORMATION:
		APPLICANT: YAN, Chunhua et al.
		TITLE OF INVENTION: ISOLATED HUMAN LIPASE PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN LIPASE PROTEINS, AND
		TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN LIPASE PROTEINS, AND
		TITLE OF INVENTION: THEREOF.
		FILE REFERENCE: CL001170
		CURRENT APPLICATION NUMBER: US/09/811-820
		CURRENT FILING DATE: 2001-03-20
		CURRENT APPLICATION NUMBER: US/09/811-825
		CURRENT FILING DATE: 2001-03-20

```

NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 2
LENGTH: 398
TYPE: PRT
ORGANISM: Human
US-09-811-825-2

Query Match 88.6%; Score 1991; DB 10; Length 398;
Best Local Similarity 100.0%; Pred. No. 5.1e-180; Mismatches 0; Indels 0; Gaps 0;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 50 SEI.IQHGYPOEYEVATEDYIISNRPICLQVQPKTKTSRPVYVLLQHGLYGGASWIS 109
Db 25 SEI.IQHGYPOEYEVATEDYIISNRPICLQVQPKTKTSRPVYVLLQHGLYGGASWIS 84
Qy 110 NLPNNSLGFILADAGFDWMGNRSRGNASRAHKTLSDQDEFWAFSYDEMARFDLPAVIN 169
Db 85 NLPNNSLGFILADAGFDWMGNRSRGNASRAHKTLSDQDEFWAFSYDEMARFDLPAVIN 144
Qy 170 FILQTKQEIKIYVGYSQGTMTGFIATFSTMPLEAOKITKMFALAPIATVKHAKSPGCKFL 229
Db 145 FILQTKQEIKIYVGYSQGTMTGFIATFSTMPLEAOKITKMFALAPIATVKHAKSPGCKFL 204
Qy 230 LLPDMMIKGLGKKEFYQTRFLQVLYTLCQVILQDQCSNIMLIGGENTNNMNSRA 289
Db 205 LLPDMMIKGLGKKEFYQTRFLQVLYTLCQVILQDQCSNIMLIGGENTNNMNSRA 264
Qy 290 SV^AAHTLAGT^VQNLHWSQAVNSGELAFDGMGSETKNLERKCNQPTPVRYVRDMTVP^T 349
Db 265 SV^AAHTLAGT^VQNLHWSQAVNSGELAFDGMGSETKNLERKCNQPTPVRYVRDMTVP^T 324
Qy 350 AMNTGGDWMSPEDYKMLLSEVTNLHYKNIPEWAHDFINGLDAPHRYMENEIHLMOQ 409
Db 325 AMNTGGDWMSPEDYKMLLSEVTNLHYKNIPEWAHDFINGLDAPHRYMENEIHLMOQ 384
Qy 410 EETNLSQGRCAEVL 423
Db 385 EETNLSQGRCAEVL 398

RESULT 6
US-10-042-431-41
Sequence 41, Application US/10042431
Publication No. US20020182675A1
GENERAL INFORMATION:
APPLICANT: MCCARTHY, Sean A
APPLICANT: BARNES, Thomas M
APPLICANT: FRASER, Christopher C
APPLICANT: SHARP, John D
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC, THERAPEUTIC, AND OTHER USES
TITLE OF INVENTION: PREVENTIVE, THERAPEUTIC, AND OTHER USES
FILE REFERENCE: 10147-602
CURRENT APPLICATION NUMBER: US/10/042,431
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: US 09/333,159
PRIOR FILING DATE: 1999-06-14
PRIOR APPLICATION NUMBER: US 09/578,063
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 79
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 41
LENGTH: 399
TYPE: PRT
ORGANISM: Homo sapiens
US-10-042-431-41

Query Match 57.4%; Score 1289; DB 9; Length 399;
Best Local Similarity 63.5%; Pred. No. 8.4e 114;
Matches 235; Conservative 55; Mismatches 80; Indels 0; Gaps 0;

```

Db	28	AVDPETNMNVSEIIISYWGFPSEEEYLVETEDGYILCLNRPHGRKHNHSKGPKPKPVFLQHG	87	Db	326	YNYKDMLYPTAVWGGHHDWLADYDVNILLTQTINLYFHESTIPEWEHLDFFWGLDAPWRL	385
Qy	100	LVGGASWISLNPSLNGFILADAGFDWMGNSRGNASWRKHTLSIDQDEFWAFSYDEM	159	Qy	400	YNBIIHL'406	
Db	88	LLADSSWVNTLNANSSLGFILADAGFDWMGNSRGNASWRKHTLSIDQDEFWAFSYDEM	147	Db	386	YNIKINL'392	
Qy	160	ARFDLPAVINFLQKTCQEKKIYVYGSQGTMGFIASFSTMPLEAKIKMYPALAPIATVK	219				
Db	148	AKYDLPASINFLNKTGQEVYVGHSGQTIGFIAFSQIPELAKRIMKFFALGPVAVSA	207				
		RESULT 8					
Qy	220	HAKSPGCKFLLPDMMIKGLGKKEFLYQTRFLQVYILCGQVILDOICSNIMLLGGF	279				
Db	208	FCTSPMAKLRGPFLDHLKDLDFKDELPQSAFLKWLQGTHVILKELCGNLUFLCGF	267				
Qy	280	NTNNMNMRSASYAAHTLAGTSVQNLHWSQAVNSGLRAFDWGSETPKNLEKCNQPPPVR	339				
Db	268	NERLNKNSRVDVYTHSPAGISVQNLHWSQAVKFKQAFDWGSSETPKNLEKCNQPPPVR	327				
Qy	340	YRVRDWTPTAMWGGDWLSNPEDYKMLLSEVTNLYIYHKNIPEWAHDFIWGLDAPHRM	399				
Db	328	YVKDMLVPTAWSGHDLADYDVNILLQTINLYFHESTIPEWEHLDFFWGLDAPWRL	387				
Qy	400	YNEIYHEMQQ 409					
Db	388	YNIKINLMRK 397					
		RESULT 7					
US-10-003-302-4		Score 57.1%; Pred. No. 3.8e-113; Mismatches 53; Gaps 0; Indels 0; Gaps 0;					
Patent No. US20020142435A1		Sequence 4, Application US/10003302 .					
GENERAL INFORMATION		Sequence 50, Application US/10042431 .					
APPLICANT: MERKULOV, Gennady et al.		Publication No. US20020182675A1					
TITLE OF INVENTION: ISOLATED HUMAN LIPASE PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN LIPASE PROTEINS, AND USES		GENERAL INFORMATION:					
FILE REFERENCE: CL00118DDIV		APPLICANT: MCCARTHY, Sean A.					
CURRENT APPLICATION NUMBER: US/10/003,302		APPLICANT: BARNES, Thomas M.					
CURRENT FILING DATE: 2001-12-06		APPLICANT: FRASER, Christopher C.					
NUMBER OF SEQ ID NOS: 4		APPLICANT: SHAREF, John D.					
SEQ ID NO 4		TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC, THERAPEUTIC, AND OTHER USES					
SOFTWARE: FASTSEQ for Windows Version 4.0		FILE REFERENCE: 10147-602					
LENGTH: 392		CURRENT APPLICATION NUMBER: US/10/042,431					
TYPE: PRT		CURRENT FILING DATE: 2001-10-25					
ORGANISM: Homo sapiens		PRIOR APPLICATION NUMBER: US 09/333,159					
US-10-003-302-4		PRIOR FILING DATE: 1999-06-14					
		PRIOR APPLICATION NUMBER: US 09/578,063					
		PRIOR FILING DATE: 2000-05-24					
		NUMBER OF SEQ ID NOS: 79					
		SOFTWARE: Patentin Ver. 2.1					
		SEQ ID NO 50					
		LENGTH: 221					
		TYPE: PRT					
		ORGANISM: Homo sapiens					
		US-10-042-431-50					
		Query Match 51.8%; Score 1165; DB 9; Length 221;					
		Best Local Similarity 100.0%; Pred. No. 1.8e-102; Mismatches 0; Indels 0; Gaps 0;					
		Matches 221; Conservative 0; Gaps 0;					
		GENERAL INFORMATION:					
		APPLICANT: MCCARTHY, Sean A.					
		APPLICANT: BARNES, Thomas M.					
		APPLICANT: FRASER, Christopher C.					
		APPLICANT: SHAREF, John D.					
		TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC, THERAPEUTIC, AND OTHER USES					
		FILE REFERENCE: 10147-602					
		CURRENT APPLICATION NUMBER: US/10/042,431					
		CURRENT FILING DATE: 2001-10-25					
		PRIOR APPLICATION NUMBER: US 09/333,159					
		PRIOR FILING DATE: 1999-05-14					
		PRIOR APPLICATION NUMBER: US 09/578,063					
		PRIOR FILING DATE: 2000-05-24					
		NUMBER OF SEQ ID NOS: 79					
		RESULT 9					
US-10-042-431-75		Score 57.1%; Pred. No. 3.8e-113; Mismatches 53; Gaps 0; Indels 0; Gaps 0;					
Best Local Similarity 63.8%; Pred. No. 3.8e-113; Mismatches 53; Gaps 0; Indels 0; Gaps 0;		Sequence 75, Application US/10042431 .					
Matches 234; Conservative 0; Gaps 0;		Publication No. US20020182675A1					
SOFTWARE: AVDPETNMNVSEIIISYWGFPSEEEYLVETEDGYILCLNRPHGRKHNHSKGPKPKPVFLQHG	85						
Db	26	AVDPETNMNVSEIIISYWGFPSEEEYLVETEDGYILCLNRPHGRKHNHSKGPKPKPVFLQHG	85				
Qy	100	LVGGASWISLNPSLNGFILADAGFDWMGNSRGNASWRKHTLSIDQDEFWAFSYDEM	159				
Db	86	LLADSSWVNTLNANSSLGFILADAGFDWMGNSRGNASWRKHTLSIDQDEFWAFSYDEM	145				
Qy	160	ARFDLPAVINFLQKTCQEKKIYVYGSQGTMGFIASFSTMPLEAKIKMYPALAPIATVK	219				
Db	146	AKYDLPASINFLNKTGQEVYVGHSGQTIGFIAFSQIPELAKRIMKFFALGPVAVSA	205				
Qy	220	HAKSPGCKFLLPDMMIKGLGKKEFLYQTRFLQVYILCGQVILDOICSNIMLLGGF	279				
Db	206	FCTSPMAKLRGPFLDHLKDLDFKDELPQSAFLKWLQGTHVILKELCGNLUFLCGF	265				
Qy	280	NTNNMNMRSASYAAHTLAGTSVQNLHWSQAVNSGLRAFDWGSSETPKNLEKCNQPPVR	339				
Db	266	NERLNKNSRVDVYTHSPAGISVQNLHWSQAVKFKQAFDWGSSETPKNLEKCNQPPVR	325				
Qy	340	YRVRDWTPTAMWGGDWLSNPEDYKMLLSEVTNLYIYHKNIPEWAHDFIWGLDAPHRM	399				

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-042-431-75

Query Match 49.8%; Score 1119; DB 9; Length 398;
Best Local Similarity 52.8%; Pred. No. 9.1e-98;
Matches 210; Conservative 73; Indels 12; Gaps 2;

Qy 17 MWLILVAYMFORVNVSVHMPTKAV-----DEPEAMNINISIHQGYPCEBEYATED 69
Db 1 MWLLLTMASLI----SVLGTHGFLGKHLPGSPPEVNTNISOMITYWGPMEYEYTED 55

Qy 70 GYILSYNRPPIRGLVQPKRTGSPRVVYIQLHGLYGGASNWISLPNNSLGFFILADAGFDWW 129
Db 56 GYILEVNRPPIRGPKKSNTGQRPVFVQHGLLASAWNISLPNNSLAFLADAGDWWL 115

Qy 130 GNSRGNAWSRKHKTLSIDQDEFWAFSYDEMARFDLPAVINELIQLTQKEIYVGSQQT 189
Db 116 GNSRGNTWARRNLYSSPDSVERWAFSYDEMARFDLPAVINELIQLTQKEIYVGSQQT 175

Qy 190 TMGFIATSTMPLEAQKIKMYFALAPTVKHKASPGTKFLLPDMMIKGLFGKKEFYQT 249
Db 176 TIGFIATSTNPSLAKRKTFYALAPTVKTKSLINKLRFVPOSLEKFIFGDKIPYPHN 235

Qy 250 RFLRQLVYIQLCGQVILDOICNSIMLJGFGNTNNMNSRASVYAAUTLAGTSVQNTLHWS 309
Db 236 FFFQFLATEVCSEMLNLCWALFICGFDSKNFNTSRDLYLSPNAGTSVQNNFHWL 295

Qy 310 QAVNSGELRAFDGSEKVNLEKCNQPPVVRVDMVPTAMWTGODWLSNPEDYKML 369
Db 296 QAVKSGRFQAYDGGSPVQNRHYDOSQUPPYINTAANVTPAIVNGKRDLLADPQDYLIL 355

Qy 370 SEVTNLVYHKNIPPEAWHDFWGLDAFRHMYNEIILHMQQE 411
Db 356 PKLPNLVYHKEIPYNHLDIFWAMDAEQVNDIVSMEED 397

RESULT 10
; Sequence 2, Application US/10056744B
; Publication No. US2002103303A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: 58850, A HUMAN CHOLESTERYL ESTER
; TITLE OF INVENTION: HYDROLASE AND USES THEREFOR
; FILE REFERENCE: MP12001-026P1RM
; CURRENT APPLICATION NUMBER: US/10/056,744B
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 60/264,167
; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-056-744B-2

Query Match 48.5%; Score 1090; DB 9; Length 398;
Best Local Similarity 5.4%; Pred. No. 5e-95;
Matches 207; Conservative 61; Indels 4; Gaps 2;

Qy 17 MWLILVAYMFORVNVS--VHMPTKAVDPEAMNINISIHQGYPCEBEYATEDYIYL 73
Db 2 MWLLLTCLICGTLNAGGFDLNE-VNPETWANTSBEIINGYPPEBEYETTYDYIYL 60

Qy 74 SVNRIPRGLVQPKRTGSPRVVYIQLHGLYGGASNWISLPNNSLGFFILADAGFDWW 133
Db 61 LVNRIPRGRTHARSTGPRVYVQHGLYGGASNWLENYANGSLGFFILADAGTDYMGNSR 120

Qy 134 GNSRGNAWSRKHKTLSIDQDEFWAFSYDEMARFDLPAVINELIQLTQKEIYVGSQQT 193
Db 121 GNSRGNTWARRNLYSSPDSVERWAFSYDEMARFDLPAVINELIQLTQKEIYVGSQQT 180

Qy 194 TAPSTMPLEAQKIKMYFALAPTVKHKASPGTKFLLPDMMIKGLFGKKEFYQTFRFLR 253
Db 181 VAPSTMPLEAQKIKMYNQSHSPPYDITAMVPTAIVGGLDAPHRMYN 401

Qy 254 QLVYLQCGOVIDOICNSIMLJGFGNTNNMNSRASVYAAUTLAGTSVQNTLHWSQAVN 313
Db 241 TAPSTKICNKKLWICSEMSLWAGSNKNNQSRDYMMSHAPGSSVHNHLIKOLYH 300

Qy 314 SGPLRAFDGSEKVNLEKCNQPPVVRVDMVPTAMWTGODWLSNPEDYKMLSEVT 373
Db 301 SDIFRATDWGNDADNMKHYNQSHSPPYDITAMVPTAIVGGLDAPHRMYN 360

Qy 374 NL-IYHKNIPENAHV-DRIWGLDAPHRMYN 401
Db 361 SLSLVLSLUPWNPPTFDFWGLDAPORMFS 390

RESULT 12
 US-10-042-431-52
 ; Sequence 52, Application US/10042431
 ; Publication No. US20020182675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MCCARTHY, Sean A
 ; APPLICANT: BARNES, Thomas M
 ; APPLICANT: FRASER, Christopher C
 ; APPLICANT: SHARP, John D
 ; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,
 ; FILE REFERENCE: 10147-602
 ; CURRENT APPLICATION NUMBER: US/10/042,431
 ; CURRENT FILING DATE: 2001-10-25
 ; PRIOR APPLICATION NUMBER: US 09/333,159
 ; PRIOR FILING DATE: 1999-06-14
 ; PRIOR APPLICATION NUMBER: US 09/578,063
 ; PRIOR FILING DATE: 2000-05-24
 ; NUMBER OF SEQ ID NOS: 79
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 52
 ; LENGTH: 144
 ; ORGANISM: Homo sapiens
 ; US-10-042-431-52

Query Match 34.8%; Score 783; DB 9; Length 144;
 Best Local Similarity 100.0%; Pred. No. 1.1e-66; Indels 0; Gaps 0;
 Matches 144; Conservative 0; Mismatches 0; SEQ ID NO: 48

Qy 280 NTNNNNMSRASVYAAHTLAGTSVQNLHNSQAVNSGELRAFDKGSETKNEKCNOPTPVR 339
 Db 1 NTNNNNMSRASVYAAHTLAGTSVQNLHNSQAVNSGELRAFDKGSETKNEKCNOPTPVR 60

Qy 340 YRVRDMDTVPTAMWTTGGQDNLSPEDVKMILSEVNTLHYHKNIPERAHYDFIWGLDAPHM 399
 Db 61 YRVRDMDTVPTAMWTTGGQDNLSPEDVKMILSEVNTLHYHKNIPERAHYDFIWGLDAPHM 120

Qy 400 YNEI1HLMQDEETNLNSQGRCEAVL 423
 Db 121 YNEI1HLMQDEETNLNSQGRCEAVL 144

RESULT 13
 US-10-056-744-B-5
 ; Sequence 5, Application US/10056744B
 ; Publication No. US20020193303A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kapeller-Libermann, Rosana
 ; TITLE OF INVENTION: 58860, A HUMAN CHOLESTERYL ESTER
 ; TITLE OF INVENTION: HYDROLASE AND USES THEREFOR
 ; FILE REFERENCE: MPI2001-02SP1RN
 ; CURRENT APPLICATION NUMBER: US/10/056,744B
 ; CURRENT FILING DATE: 2002-08-16
 ; PRIOR APPLICATION NUMBER: 60/264,167
 ; PRIOR FILING DATE: 2001-01-25
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 5
 ; LENGTH: 127
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-056-744-B-5

Query Match 17.8%; Score 400; DB 9; Length 127;
 Best Local Similarity 58.5%; Pred. No. 1.2e-10; Indels 0; Gaps 0;
 Matches 72; Conservative 22; Mismatches 29; SEQ ID NO: 51

Qy 107 WISNPNNSLGSFILADAGFDVWGNNSRGNAWSRKKHTLSDQDEFAFSYDEARFDLPA 166
 Db 1 WIANGENKNSLAFLADAGDYLWLNRSRGNTYSRKHYKLNPSPHSEFDSNHEMGMYDLPA 60

RESULT 14
 US-10-042-431-48
 ; Sequence 48, Application US/10042431
 ; Publication No. US20020182675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MCCARTHY, Sean A
 ; APPLICANT: BARNES, Thomas M
 ; APPLICANT: FRASER, Christopher C
 ; APPLICANT: SHARP, John D
 ; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,
 ; TITLE OF INVENTION: PREVENTIVE, THERAPEUTIC, AND OTHER USES
 ; FILE REFERENCE: 10147-602
 ; CURRENT APPLICATION NUMBER: US/10/042,431
 ; CURRENT FILING DATE: 2001-10-25
 ; PRIOR APPLICATION NUMBER: US 09/333,159
 ; PRIOR FILING DATE: 1999-06-14
 ; PRIOR APPLICATION NUMBER: US 09/578,063
 ; PRIOR FILING DATE: 2000-05-24
 ; NUMBER OF SEQ ID NOS: 79
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 48

Query Match 7.6%; Score 171; DB 9; Length 33;
 Best Local Similarity 100.0%; Pred. No. 7.2e-10; Indels 0; Gaps 0;
 Matches 33; Conservative 0; Mismatches 0; SEQ ID NO: 48

Qy 1 MLETLSRQWTVSHRMEMWLLILVAYMFQRNVNS 33
 Db 1 MLETLSRQWTVSHRMEMWLLILVAYMFQRNVNS 33

RESULT 15
 US-10-042-431-51
 ; Sequence 51, Application US/10042431
 ; Publication No. US20020182675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MCCARTHY, Sean A
 ; APPLICANT: BARNES, Thomas M
 ; APPLICANT: FRASER, Christopher C
 ; APPLICANT: SHARP, John D
 ; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,
 ; TITLE OF INVENTION: PREVENTIVE, THERAPEUTIC, AND OTHER USES
 ; FILE REFERENCE: 10147-602
 ; CURRENT APPLICATION NUMBER: US/10/042,431
 ; CURRENT FILING DATE: 2001-10-25
 ; PRIOR APPLICATION NUMBER: US 09/333,159
 ; PRIOR FILING DATE: 1999-06-14
 ; PRIOR APPLICATION NUMBER: US 09/578,063
 ; PRIOR FILING DATE: 2000-05-24
 ; NUMBER OF SEQ ID NOS: 79
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 51
 ; LENGTH: 25
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-042-431-51

Query Match 5.7%; Score 128; DB 9; Length 25;
 Best Local Similarity 100.0%; Pred. No. 5.5e-06; Indels 0; Gaps 0;

Qy 255 LVIYLGGVILDQICSNIMLLGGF 279
Db 1 LVIYLGGVILDQICSNIMLLGGF 25

Search completed: February 3, 2003, 13:54:11
Job time : 14 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 3, 2003, 13:47:54 ; Search time 21 Seconds
(without alignments)
1936.422 Million cell updates/sec

Title: US-09-333-159-47
Perfect score: 2247
Sequence: 1 MLETLSROWIVSHRMEMVLL.....IHLMQQEETNLISQGRCPAVL 423

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database : PIR73:*

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	1290	lysosomal acid lipase	lysosomal acid lip	57.4	S4108	lysosomal acid lip
2	1290	lysosomal acid lipase	lysosomal acid lip	57.4	S4108	lysosomal acid lip
3	1164.5	triaxylglycerol	triaxylglycerol	51.8	G01416	triaxylglycerol
4	1139	triaxylglycerol	triaxylglycerol	50.7	LIRPT	triaxylglycerol
5	1119	triaxylglycerol	triaxylglycerol	49.8	JC017	triaxylglycerol
6	752.5	hypothetical protein	hypothetical protein	33.5	S07145	hypothetical protein
7	751	hypothetical protein	hypothetical protein	33.4	T33198	hypothetical protein
8	730	hypothetical protein	hypothetical protein	32.5	T22275	hypothetical protein
9	707.5	hypothetical protein	hypothetical protein	31.5	405	hypothetical protein
10	692	hypothetical protein	hypothetical protein	30.8	H88930	hypothetical protein
11	655.5	hypothetical protein	hypothetical protein	29.8	411	hypothetical protein
12	574.5	hypothetical protein	hypothetical protein	25.6	426	hypothetical protein
13	505	hypothetical protein	hypothetical protein	22.5	T20480	hypothetical protein
14	478.5	hypothetical protein	hypothetical protein	21.3	T22290	hypothetical protein
15	475	hypothetical protein	hypothetical protein	21.1	T4153	hypothetical protein
16	445	hypothetical protein	hypothetical protein	19.8	E84326	hypothetical protein
17	422.5	hypothetical protein	hypothetical protein	18.8	S37969	hypothetical protein
18	412.5	hypothetical protein	hypothetical protein	18.4	460	hypothetical protein
19	411.5	hypothetical protein	hypothetical protein	18.3	T39443	hypothetical protein
20	294	hypothetical protein	hypothetical protein	13.1	T41540	hypothetical protein
21	285	hypothetical protein	hypothetical protein	12.7	538	hypothetical protein
22	271.5	hypothetical protein	hypothetical protein	12.1	S64942	hypothetical protein
23	234.5	hypothetical protein	hypothetical protein	10.4	509	hypothetical protein
24	149	hypothetical protein	hypothetical protein	6.6	S59904	hypothetical protein
25	143	hypothetical protein	hypothetical protein	6.4	336	hypothetical protein
26	126	hypothetical protein	hypothetical protein	5.6	F8325	hypothetical protein
27	113	hypothetical protein	hypothetical protein	5.0	A64474	hypothetical protein
28	112.5	hypothetical protein	hypothetical protein	5.0	B72291	hypothetical protein
29	107	hypothetical protein	hypothetical protein	4.8	S19339	hypothetical protein

ALIGNMENTS

30	105.5	4.7	304	2	A89905	hypothetical protein
31	103.5	4.7	430	2	T2001	hypothetical protein
32	101.5	4.5	798	2	F96714	probable protease
33	101	4.5	929	2	JH0262	OutR protein - Eme
34	99.5	4.5	436	2	JC5021	platelet-activatin
35	99.5	4.4	286	2	D7217	probable 2'-acetyl-
36	99.5	4.4	1280	2	B34087	hypothetical prote
37	99	4.4	318	2	F98114	probable permease
						ABC transporter, m
						unprotein
						R; Ames, D.; Merk, M.; Eckers, C.; Greten, H.
						Eur. J. Biochem. 219, 905-914, 1994
						A; Title: Purification, characterization and molecular cloning of human hepatic lysosomal acid lipase/chole
						ester transcriptase
						probable membrane
						DNA polymerase I

RESULT 1						
S41408	lysosomal acid lipase (EC 3.1.1.1) / sterol esterase (EC 3.1.1.13) precursor - human					
C; Species: Homo sapiens (man)						
C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 18-Jun-1999						
C; Accession: S41408; A39315; S47187						
R; Anderson, R.A.; Sando, G.N.						
J. Biol. Chem. 266, 22479-22484, 1991						
A; Title: Cloning and expression of cDNA encoding human lysosomal acid lipase/chole						
A; Reference number: A39315; MUID: 94155897; PMID: 8112342						
A; Accession: S41408						
A; Status: preliminary						
A; Molecule type: mRNA						
A; Residues: 1-15, 'P', 17-399 <AND>						
A; Cross-references: EMBL: X76488; PIDN: 9434305; PIDN: AAA59519.1; PMID: 9434306						
R; Du, H.; Gregory, G.A.						
submitted to the EMBL Data Library, April 1994						
A; Description: Structural conservation of putative functional motifs between mouse						
A; Reference Number: S47187						
A; Accession: S47187						
A; Status: preliminary						
A; Molecule type: mRNA						
A; Residues: 1-22, 'R', 24-399 <DUH>						
A; Cross-references: EMBL: Z31690; PIDN: 9506430; PIDN: AAA83495.1; PMID: 9506431						
A; Map Position: 10q24-10q25						
C; Superfamily: triacylglycerol lipase, lingual						
C; Keywords: carboxylic ester hydrolase, glycoprotein						
C; Genetics:						
A; Gene: GDB: LIP A						
A; Cross-references: GDB: 120153; OMIM: 278000						
A; Map Position: 10q24-10q25						
Matches 24/2; Conservativeness 59; Mismatches 94; Indels 2; Gaps 1;						
Qy 15 MEWLLLTLVAYMQRNVNSVHMRPTK - AYDPEEPMNTEIIQHGPPEYEVATEDGYI 72						
Db 1 MKMRFLGLVVCLVLLWTHSEGSGKLZAVDPDTNMVSEIIWSWGFSESEYLVETEDGYI 60						
Query Match 57.4%; Score 1290; DB 2; Length 399;						
Best Local Similarity 61.0%; Pred. No. 1-86-105;						
Matches 24/2; Conservativeness 59; Mismatches 94; Indels 2; Gaps 1;						
Qy 15 MEWLLLTLVAYMQRNVNSVHMRPTK - AYDPEEPMNTEIIQHGPPEYEVATEDGYI 72						
Db 1 MKMRFLGLVVCLVLLWTHSEGSGKLZAVDPDTNMVSEIIWSWGFSESEYLVETEDGYI 60						
Query 73 LSVNRPTRPLQVPPKKTGSRPVYLLQHGLVGGASWISNLPNNSLGLFTLADAGFDVWGNNS 132						
Db 61 LCNRIPHGRKHNSDGPKPVYFLQHGLLADASWVNTLANSGLFTLADAGFDVWGNNS 120						

Y	133	RGNAWSRKHTLISDQDEFWASYDENARDFPAVINELIORTGQERKIYTYGSQSTGTMG	192
Y	121	RGNTRWSRKHTLISDQDEFWASYDENARDFPAVINELIORTGQERKIYTYGSQSTG	180
Y	193	FIAFSTMPLEAQKIKMYFALAPATYKHKASPGTKEPLLPPDMMIKGFLGKKEFELYQTRFL	252
Y	181	FIAFSQLPELARIKRMFALPGVASTAFCTSEMAKJGRPLPHLIDQFLGDFREFLPOSAFL	240
Y	253	ROLVIVLGQVILDOIICNSNIMLILGGFTNTNNMMSRASYAHTLAGTSVONLILMSQAV	312
Y	241	KVLGTHVCTHVKLGNCNLFLACGFERNLNMSRVDYTTHSPAGTSQNLMHSQAV	300
Y	313	NSGELRAFDWGSETRNIEJKCROPTPYRYVRDMTVPTAMTGGDMLSNPBDVKMULSEV	372
Y	301	KFQKQAFDWGSSAKNYPHYNOSPPTYNVRDMLVPTAVWSGGHDLADYDVNLILTQI	360
Y	373	TNLJYHKNPENAHVDTIWGLDAPHRMNEYETIHLIMQO	409
Y	361	TNLJYHKNPENAHVDTIWGLDAPHRMNEYETIHLIMQKINLMLRK	397

RESULT 2
PID:41416
triglyceridic acid lipase - human
Species: Homo sapiens (man)
Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 18-Jun-1999
Accession: G01416
Dui, H.
Submitted to the EMBL Data Library, April 1994
Reference number: G06919
Accession: G01416
Status: preliminary; translated from GB/EMBL/DDBJ
Molecule type: mRNA
Residues: 1-399 <DNU>
Cross references: EMBL:U08464; NID:9505052; PIDN:AA860328.1; PID:g505053
Subfamily: tracyglycerol lipase, lingual
Keywords: glycoprotein

Query	Match	Score	DB	Length
Query Match	Y	57.4%	Score 1290;	Length 399;
Best Local Similarity	Y	61.0%	Pred. No. 1. 8e-105;	
Matches 242;	Y	Conservative	Mismatches 94;	
Matches 242;	Y	242;	Indels 2;	Gaps
15	MEMWILLYAVMFQRNYYNSVHMPKT -	AVDPEAFMNTSEITOHOGYPCEEVEYEVATEDGYI	72	
1	MKHFRFLGIVLVLWTHSEGSRGKLTAVDPTNMAYSEITSYWGFSEEEVLVETDGYI	60		
73	LSVNIRIPRGVLQVQPKTKTSSRPVYLLQRLVYGGASNWTISNLPNNSLGFLLADAGFDVGMGNS	132		
61	LCLNIRIPGRKHNHSKGPKPVYFLQHGLLADSNNYTNLANSLGFLLLADAGFDVGMGNS	120		
133	RGNAWSRKHTLSIDQDDEFWAFSYDENARFDLPAVINFLQRTQKEXIYYGGSQGTTMG	192		
121	RGNITWSRKHTLSSQDEFWAFSYDENAKYDLPASINFLNKTGQEQQVYGHSGQTG	180		
193	FIAFSTMMPLEAQKIMYFALAPATVYHAKSPGTKFVLLPDMMIKGLFGKKEFLYQTRFL	252		
181	FIAFSQIPBLAKRKMFPALGPVAVSFECTSPMAKLRLPDLIKDFGDFEFLPOSAFL	240		
253	RQLYIVLGQVILDQICNSIMLIGGFTNNNNMSRSVYAAHTLACTSVQNLHRSQAV	312		
241	KWLGHVCTHVKELCNCNLFCFLCGFERNLNMSMSRVDVYATHSPACTSVQNLHRSQAV	300		
313	NSGELRDPDGSETKLNKLCNCFPLCGFERNLNMSMSRVDVYATHSPACTSVQNLHRSQAV	372		
301	KFQKFOADWGSSAAKNFHYNQSPPTYNVKOMLVPFAVWSGHDWLADEVYNVNLITLQI	360		
373	TNLVYHKNTPENWHDFTWGLDAPRHYNEITLHMQQ	409		
361	TNLVWHESTPEWHLDFTWGLDAPRHYNEITLHMQQ	397		

triaxylglycerol lipase (EC 3.1.1.3) precursor, lingual - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 11-Jun-1
 C;Accession: A23045
 R;Docherty, A.J.P.; Bodmer, M.W.; Angal, S.; Verger, R.; Riviere, C.; Lo
 Nucleic Acids Res. 13, 1891-1903, 1985
 A;Title: Molecular cloning and nucleotide sequence of rat lingual lipase
 A;Reference number: A23045; MUID:85215587; PMID:3839077
 A;Accession: A23045
 A;Molecule type: mRNA
 A;Residues: 1-395 <DOC>
 A;Cross-references: GB:U03309; NID:956595; PID:CA26179.1; PID:56596
 A;Experimental source: strain Sprague-Dawley
 A;Note: the partial sequence of the mature protein from a different, unsi
 C;Comment: This acid-stable lipase is secreted by the serous (von Ebner's)
 C;Superfamily: triacylglycerol lipase, lingual
 C;Keywords: carboxylic ester hydrolase; glycoprotein; lipid digestion; s
 F;1-187/domain: signal sequence #status predicted <S>
 F;19-395/Product: triacylglycerol lipase, lingual #status predicted <S>
 F;P;33,68,98,184,270/binding site: carbohydrate (Asn) (covalent) #status p

RESULT 3

C:/Keywords: carboxylic ester hydrolase; extracellular protein; glycoprotein; lipid F:/1-19/Domain: signal sequence #status predicted <SIG> F:/20-398/Product: triacylglycerol lipase, gastric #status experimental <DAT> F:/30,99,185,271/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 49 8%; Score 1119; DB 2; Length 398; Best Local Similarity 52.2%; Pred. No. 2e-90; Mismatches 73; Indels 12; Gaps 2; Matches 210; Conservative 73; Mismatches 107; Indels 12; Gaps 2;
Qy 17 MWLILVAYMFQRNVNSVIMPTKAV-----DPEAFMNISETIIOHOGYPCEEEVEVATED 69 Db 1 MWLILTMASII-----SVLGTTFLGKFLHPPGSBVTANISOMITYWPNNSLGFLIADAGFDWMM 129
Qy 70 GY11SVNTRPGLVQPKTGSRPVYVLLQHGLYGGASNVNISLNPNNSLGFLIADAGFDWMM 129 Db 56 GY11LEVNRTPYGGKNSGNTGQRPVFLQGLLASSATNWNISLNPNNSLGFLIADAGFDWMM 115
Qy 130 GNSRGNAWSRKHKTLSIDQDEFWAFSYDEMAFDPAVINFILQTKQOEKIVYGVGSGT 189 Db 116 GNSRGNTRWANRLLYSPDSEWAFSDEMAKVDLPAITDFIVYKTKGTQRLHVGHSGQT 175
Qy 190 TMGFTAFSTMPPELAQOKIMYFALAPIATVKHAKSPGTKFLPLPDMMKLGFLGKKEFLYQT 249 Db 176 TIGCFATFASPNPLKRIKTFYALAPVYKTKSFLINKLREPVQSLRFKTFGKIFYPHN 235
Qy 250 REFLRQVILYLGQVTLQDQICNSNIMLQGGFTNTNNMSRASVTAHTLLAGTSVONILHMS 309 Db 236 FFDQQLATEVCSEMLNLLGCSNALEFICGDSKVENTSRDVLVLSHNPAGTSVQNMFMHNT 295
Qy 310 QAVNSGELLRAFDWSETKKNLCKNQPTPYRVRDMTVPTAMWGGDQLLSNPEDVKMIL 369 Db 296 QAVKSGKFKQAYDWGSPVQNRMHYDQSOPPYNTAMNPYTAIWNGKDLIADPDVGVLIL 355
Qy 370 SEVTNLYIYHANIPEWAHDEIWLGDAPHRMNEYITHLMOOE 411 Db 356 PKJPNLIIYKKEPFPYIHLDFIWADAPQEVYNDIVSMEEDK 397
Db
RESULT 6
T3 3198 hypothetical protein ZK6.7 - <i>Caenorhabditis elegans</i>
C:Species: <i>Caenorhabditis elegans</i>
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jan-2000
C:Accession: T3198
R:Wu, X.
submitted to the EMBL Data Library, May 1998
A:Description: The sequence of <i>C. elegans</i> cosmid ZK6.
A:Reference number: Z21301
A:Accession: T3198
A:Status: Preliminary; translated from GB/EMBL/DDBJ
A: Molecule type: DNA
A:Residues: 1-403 <NWX>
A:Cross-references: EMBL:AF067942; PIDN: AAC17694.1; GSPDB:GN00023; CBSP:2K6.7
A:Experimental source: strain Bristol N; Clone ZK6
C:Genetics:
A:Gene: CESP:ZK6.7
A:Map position: 5
A:Introns: 29/3; 63/1; 219/3; 319/3; 365/3
C:Superfamily: triacylglycerol lipase, lingual
Query Match 33.5%; Score 752.5; DB 2; Length 403; Best Local Similarity 41.1%; Pred. No. 3.5e-58; Mismatches 66; Indels 142; Gaps 33; Gaps 12; Matches 168; Conservative 5; Mismatches 66; Indels 142; Gaps 33; Gaps 12;
Qy 17 MW-LLIVAYMFQRNVNSVIMPTKAVDPEAFMNISETIIOHOGYPCEEEVEVATEDGYILSV 75 Db 1 MRKFAFLAAEYVQPKKTT-----GSPRVPVLLQHGLYGGASNVNISLNPNNSLGFLIADAGFDWMM 129
Qy 76 NRPGLVQPKKTT-----GSPRVPVLLQHGLYGGASNVNISLNPNNSLGFLIADAGFDWMM 129 Db 56 HRIPFG-----KTNVTPNGKRPVYEMQHGLCASSDWVYNLPDOSAGFLFADAGFDWMM 110
Qy 130 GNSRGNAWSRKHKTLSIDQDEFWAFSYDEMAFDPAVINFILQTKQOEKIVYGVGSGT 189

Db	111	GNMRGNTYSMRRHKDKLPKPSHAFWDSWDEMAYTDLNAMINHVLEVGTQDSYYGMHSQGT	170	RESULT 8
Qy	190	TMGFIAFSTMP-ELAQKIKMYFALAPIATYKHAKSPGTKLPPDMIKG--LFGKKEF	245	hypothetical protein F54F3.3 - Caenorhabditis elegans
Db	171	LTMFSLHSLKDGDFAKKKFALAPGAVKNIKSPFLSTPAHKFSPEDDWYELFGSKDPLPD	230	C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999	#sequence_revision 15-Oct-1999	#text_change 21-Jan-2000	C;Accession: T22675	
C;Accession: T22675	R;Percy, C.; Lloyd, C.			
Qy	246	LYQTRELRQLVYLGGQVILD-QICSNIMLLGGNTNNMMMSRASYAAHTLAGTSVQN	304	submitted to the EMBL Data Library, September 1996
Db	231	LPNNQAVNMLAKKDCIGGKVKADLQDNVLFLIAGPESDQWQTRPVYATIDPAGSTQN	290	A;Reference number: Z19598
Qy	305	ILHWSQAVNSGELRQFADWGSSETKLNLEKCNQPTPVRYTFRVDRMT---VPTA	360	A;Accession: T22675
Db	291	WMMQMVHHGGPAIDWGKT-NKKYQGANPPEY--DETAIKGTKILYWSADWLA	346	A;Status: preliminary; translated from GB/EMBL/DBJ
Qy	361	NPDEVY-KMMLSEVTVNLYHKN--IPENWAHVDIETWGLDAPHMYNEIHL	406	A;Molecule type: DNA
Db	347	DTPDVPDYLLTRLNPAIVAQNNHLPDYNHLDETWGLRAPDDIYRPAIKL	395	A;Residues: 1-405 <WIL>
			A;Cross references: IMBL:279695; PIDN:CA01973.1; GSPDB:GN00023; CESP:F54F3.3	
			A;Experimental source: Clone F54F3	
			C;Genetics:	
			A;Gene: CESP:F54F3.3	
			A;Map position: 5	
			A;Introns: 31/3; 65/1; 274/3; 366/3	
			C;Superfamily: triacylglycerol lipase, lingual	
			Query Match 32.5%; Score 730; DB 2; Length 405;	
			Best Local Similarity 38.6%; Pred. No. 3-4e-55;	
			Matches 161; Conservative 69; Mismatches 155; Indels 32; Gaps 11;	
Qy	15	MEMWLLILVAYMFQRNVNSVHMPKTAVIDPEAFMFNISEIIOHQGYPEEEYEVATEDGILS	74	
Db	1	MRSWSWSTMLAVIATAATAVFVGH---DADPENKMTTQIMWGYPAMIDYDTEGYILE	56	
A;Species: Caenorhabditis elegans	C;Date: 15-Oct-1999	#sequence_revision 15-Oct-1999	#text_change 21-Jan-2000	C;Accession: T22675
R;McMurray, A.				
submitted to the EMBL Data Library, April 1996				
A;Reference number: Z19542				
A;Accession: T22290				
A;Status: preliminary; translated from GB/EMBL/DBJ				
A;Molecule type: DNA				
A;Residues: 1-411 <WIL>				
A;Cross references: IMBL:270780; PIDN:CAA94824.1; GSPDB:GN00023; CESP:F46B6.8				
A;Experimental source: clone F46B6				
C;Genetics:				
A;Gene: CESP:F46B6.8				
A;Map position: 5				
A;Introns: 35/3; 69/1; 104/1; 226/3				
C;Superfamily: triacylglycerol lipase, lingual				
Query Match 33.4%; Score 751; DB 2; Length 411;				
Best Local Similarity 40.4%; Pred. No. 4.9e-58;				
Matches 163; Conservative 72; Mismatches 138; Indels 30; Gaps 12;				
Qy	20	LILVAYMFQRNVNSVHMPKTAVIDPEAFMFNISEIIOHQGYPEEEYEVATEDGILSYNRI	79	
Db	10	LICRSTFLLQTINA-HPDD--DPELMNNNTSIIERGKYGAKFVHTVTEGDVILQMRIP	65	
Qy	80	RGLVQPKKT----GSRPVVILQHGLVGGASNWISLUPNNSLGFILADAGFDWNGNSR	133	
Db	66	YQ----KTSVTPWNGRPIVILQHGLACASDWVNLQPTQAAFYFADAGFDWNGNVR	120	
Qy	134	GNAWSRHKHTLSIDQDEFWAFSYDEMARFDLPAVINFQKTYQKIVYGVYSQQTGMF	193	
Db	121	GTTYGRNTKLDPSSETAFWOSWDEMAYQDPMVHLYTQVQENLYMMGHSQGTLMF	180	
Qy	194	--IAFSTMPLEAQKIKMYFALAPIATYKHAKSPGTKLPPDMIKG--LFGKEFLYQ	248	
Db	181	THLAKDGDGDFAKKKFALAPGAVKNIKSPFLSTPAHKFSPEDDWYELFGSKDPLPD	240	
Qy	249	TRFLRQLVYLGGQVILD-QICSNIMLLGGNTNNMMMSRASYAAHTLAGTSVQNILH	307	
Db	241	NNITKMAAKDCCASEKAECLDNELFLIGGPDQDNNASRPAIYSSQDPACTSTQIVH	300	
Qy	308	WSQAVNSGELRQFADWGSSETKLNLEKCNQPTPVRYTFRVDRMTVPTAMTGGDWSNPED	364	
Db	301	WQMVNRNRPADWGGKII-NKKYQGDTTPPEYDFGAIKGTI--HLYWSDDDWLGDPD	357	
Qy	365	V-KMLLSEVTVNLYHKN--PEWAHVDIETWGLDAPHMYNEII	404	
Db	358	IHDFLIKEKLNPVIAENVNKEYNHLDFWGLNATFQIYDKAI	400	
			A;Residues: 1-405 <STO>	
			A;Cross references: GB:chr-V; PIDN: AAC69088.1; GSPDB:GN00023; CESP:R11G11.14	
			A;Note: Similar to lipase; R11G11.14	
			A;Status: preliminary	
			A;Molecule type: DNA	
			C;Species: Caenorhabditis elegans	
			C;Accession: H88930	
			R;anonymous, The C. elegans Sequencing Consortium.	
			A;Title: Genome sequence of the nematode C. elegans: a platform for investigating bio	
			C;Date: 10-May-2001	#sequence_revision 10-May-2001
			C;Accession: H88930	
			A;Reference number: A75000; MURID: 99069613; PMID: 9851916	
			A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_elegans/	
			A;Accession: H88930	
			A;Status: preliminary	

C;Genetics:	118	WLGNGFRGNTYSRKIVSLSNPDKPFWDWSNDQISEYDLPAMIGKALEISGOESLYTGFPS	17
A;Gene: R1G11.14			
A;Map Position: 5			
C;Superfamily: triacylglycerol lipase, lingual			
Query Match Score 707.5; DB 2; Length 405;			
Best Local Similarity 39.0%; Pred. No. 3.2e-54;			
Matches 162; Conservative 75; Mismatches 133; Indels 45; Gaps 15;			
Qy 19 LLILVAYMFORVNVSHMPKTAVIDPEAFVNISETIQHGGPCEPPEYATEDGYLSVNR 78			
Db 9 LIVIA------VNVHHS---DPELMHMTPOIERSVPAAMTPTVYV 59			
Qy 79 PRGLVQPKKT-----GSRPVVLLQHGLGGASWNWISLNPNNSLGFILADAGFDVWGNNS 132			
Db 60 PHG-----KINVTPNGKOPPVENQHGLCATAWTMNPPEQSAFIAFADGPDWLNNS 114			
Qy 133 RGNAWSRSHKKTLSQDQEWAFSYDEMARFDLPAVINFLQKRCQEKKYVGSQG-TM 191			
Db 115 RGNTYSMKHKNLKAHSDFWENSDMAYDLPAMIDKVLTYVQESLYYMGHSQGTLM 174			
Qy 192 GFIARSTMP-----LAQKIKMYFALAPATVKAHKSPGKTFKLIPDMIKG---LFGKRE 244			
Db 175 ----FSHLSKSDDGFPAKKKFKFALAPVOSVKDKGFLSFPAHPSLSEPDGWDVFGGDE 230			
Qy 245 FLYQTRFLRQLVYLCGQV-ILDQICSNIMLLGGFNTNNMMSRASVYAAHTLAGTSVQ 303			
Db 231 2FLPNNAWKAIAKDKGKRIEIDLCDVNCFLIGPESDWNSTRPVPYASHDPAQTQ 290			
Qy 304 NLIWHSQAVNSGELAFDNGSETKNLREK-NQTPPVYRVDMT---VPTAMWGGDW 358			
Db 291 NIVHNTQMYRHGGVPAYDNGSK-ENKKVNNFOAMPPEY---DETAIKGQIYLYWSDDW 346			
Qy 359 LSNPBDV-KHLLSEVTNLHYHKN--IPEWAHDFIWGLDAPHRYNEITIHLMOQE 410			
Db 347 LADRTDTNVLTRNPRIAQNNYFTDINHDFVFGIAPRNQYLPVIDICRKD 401			
RESULT 11			
T20480 hypothetical protein F01G10_7 - Caenorhabditis elegans			
C;Species: Caenorhabditis elegans			
C;Accession: T20480 #sequence_change 15-Oct-1999 #text_change 18-Feb-20			
R;Hambry, C.			
Submitted to the EMBL Data Library, October 1996			
A;Reference number: Z19280			
A;Accession: T20480			
A;Status: preliminary; translated from GB/EMBL/DDBJ			
A;Molecule type: DNA			
A;Cross-references: <A>WIL>			
A;Experimental source: clone F01G10			
C;Genetics:			
A;Gene: CESP:F01G10_7			
A;Map position: 4			
A;Introns: 29/3; 64/1; 186/3; 347/2			
C;Superfamily: triacylglycerol lipase, lingual			
Query Match Score 29.28;			
Best Local Similarity 35.9%; Pred. No. 1.3e-49;			
Matches 140; Conservative 85; Mismatches 144; Indels 21; Gaps			
Db 20 LILWYAMFQRNVNSVHMPKTAVIDPEAFMNISEIIOHQGCPBEYEVATEDGYLSVNRIP 79			
Db 6 LFLILISFSNST-----SIAIDDEYMTPEIGRHFGESEVHLVRTDTILEHTRIP 59			
Qy 291 NIVHNTQMYRHGGVPAYDNGSK-ENKKVNNFOAMPPEY---DETAIKGQIYLYWSDDW 346			
Db 60 CKQNEKCDRSSKRPVFMQHGLLADGFSPWPNLANSQAGEYFADAGFDIWANSRTPAS 11			
Db 139 RKHKTLSIDODFWAFSYDEKARFPAVINFQIQLQKQEEVYVQYSGQTGMFIAFST 19			
Db 120 QKHIGYGPENOKFWNFTQWMSEFDLTASDVLKETKQEEPLYLGHSQGTMMFSRLAE 17			
Qy 199 MPELAQKIKMYFALAPATVKAHKSP---GTCFKLIPDMIKGFLGKKEF---LYQTRELF 25			
Db 180 NPEFAKIRIFHALAPVATSHIGGFLGFLKFLTYAEI---LGRLPSPSPSPRTV 23			
Db 253 RQLVYLGQVILDQICSNIMLLGGFNTNNMMSRASVYAAHTLAGTSVNLHHSQAV 31			
Db 236 QKMISYMCSSRFMNONCLDGFIDG-NEKMFNSQVYVLCHTPAATSYKDLQHWTQLYV 29			
Qy 313 NSGEIRAFDGSETRNLKCNQPTPVRYRDMTVTAMTGGDMLSNPDDMLLSE 37			
Db 295 KSQTVSKFDYGT-GNIEVQGPPTPEYDLOINTPTYLYWSRSDILADTOIRDLSILSK 35			
Qy 372 VTNLHYHK-NIPEWAHDFIWGLDAPHRY 400			
Db 354 MNKTAGSLPEHPSHIMDFVGTAAFDLY 38			
Query Match Score 30.8%; DB 2; Length 411;			
Best Local Similarity 36.8%; Pred. No. 7.5e-53;			
Matches 153; Conservative 83; Mismatches 154; Indels 26; Gaps 10;			
Qy 11 VSHRMEMWLLIIVMQRNVNSVHMPKTAVIDPEAFMNISEIIOHQGCPCEYEVATEDG 70			
Db 5 ISDLATMIPMLIILSNY-----SKSYDLEFLYDPELTISWGVSEVYNTTKDQ 57			
Qy 71 YLISVNRIPGLVQPKKT---GSRPVVLLQHGLGGASWNWISLNPNNSLGFILADAGFDV 127			
Db 58 FILEHRIPGREVPTSDVNNSSRPTVFLQHGFCLSSFDVANSPHQSAFVFDAGFDV 117			
Qy 128 WMGNSSRGNSRNSRKHKTLSIDOD-EFWAFSYDEKARFPAVINFQIQLQKQEEVYVQY 186			

RESULT 12

A: Residues: 1-443 <W00>
 A: Cross-references: EMBL:AL021748; PIDN:CAA16863_1; GSPDB:GN00067; SPBC16A3_12c
 A: Experimental source: strain 972h-; cosmid c16A3
 C: Genetics:

A: Gene: SPBC16A3_12c
 A: Map position: 2
 A: Introns: 11/2; 152/3; 282/1; 398/3
 C: Superfamily: triacylglycerol lipase, lingual

Query Match 22.5%; Score 505; DB 2; Length 443;
 Best Local Similarity 29.6%; Pred. No. 2.4e-36;
 Matches 125; Conservative 91; Mismatches 154; Indels 52; Gaps 13;

Qy 9 WIVSHRMEMW- LLIVAYMFORVNNSVHMPTKAVDPEAFNINSETIQHQYPCCEYEV A 66
 Db 35 YNIPERWENFVRYTLYLHYISSLTDGHTD -QKCNRIECEAFSYRVEHLVR 92

Qy 67 TEDGYTISLVRNRPGLVQPKT-GSREVVLQHGLVGASHWIS-NLPNNNLGFILADAG 124
 Db 93 TDQDNFLCLHRI---THPKQSOHKREVVYCHGLMTNSELSLWAVNESERSLPLIESG 148

Qy 125 FDWMMGNSRGNAWSRKHTLSIDDEWEWAFTSYDEMARFDUPAVINFLQKQGK1YYVG 184
 Db 149 YDWLGNRNGKNSRKHITYPKRDEEFWNFSTLDDMAMEFDIDTVDILREGREKINYIG 208

Qy 185 YSGTGTNGFLAFTSTMPMLAQIKMFALAPATVKHAKSPGTKELL--PDMMIKGFLGK 242
 Db 209 FSGTQAMALASINPDLNDKVNIFGLAPAYAPKGSFNSYFVDIYKVNPTIMYH-LFGR 267

Qy 243 KEPFLYQPRFLQVLYLQGQVLDQICSNIMMLGGFNTNNMSTASVYKAHTLAGTSV 302
 Db 268 RCLLPSVTFQN---ICYPFFVKIVDVSLSKILEWNDSLNSLNQKLCGFAHLSFSSV 323

Qy 303 ONLHNSOAVNSGELRAFD-----WGS-----TKNLERKCNQOPTPVYRVRDMT 346
 Db 324 KSVVHWLQIKNCTFQLYDDMALLAGYGSRHYQVPLFTNNI -KC----- 368

Qy 347 VPTAMWTFGGODLNSNPEDVKMILSEVNLNLYHKNIPERAWHDFINGLDAPHRMYNEIHL 406
 Db 369 -PMLIUNGKDTLINMVMYRMLPHAKEV--STAHYEHDLFLWQGDVKBEVFPVIDA 424

Qy 407 MQ 408
 Db 425 LK 426

RESULT 14

T31611 hypothetical protein Y50E8A.g - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C: Date: 29-Oct-1999
 C: sequence_revision 29-Oct-1999
 C: Accession: T31611
 R: Steward, C.
 A: Reference number: Z21047
 A: Accession: T31611
 A: Status: preliminary; translated from GB/EMBL/DBJ
 A: Molecule type: DNA
 C: Genetics:

A: Residues: 1-1585 <W11>
 A: Cross-references: EMBL:AL117200; NID:e1549770; PIDN:CAB55050_1; CESP:Y50E8A.g
 A: Introns: 25/3; 60/1; 133/2; 217/3; 337/2; 400/1; 746/2

Query Match 21.3%; Score 478.5; DB 2; Length 1585;
 Best Local Similarity 30.6%; Pred. No. 3.1e-33;
 Matches 118; Conservative 67; Mismatches 172; Indels 29; Gaps 9;

Qy 44 EAFMNISEIQHQYPCBEYEVATEDGYILSYNIRPQLVQPKKTG -SRPVVLLQHGLV 101
 Db 20 EETLDAADTISHYGYTVEKHYVTTDDGTVLQRIPIYGRDDRSILGCSKRPVVFFMHGLF 79

A: Residues: 1-443 <W00>
 A: Cross-references: EMBL:AL021748; PIDN:CAA16863_1; GSPDB:GN00067; SPBC16A3_12c
 A: Experimental source: strain 972h-; cosmid c16A3
 C: Genetics:

A: Gene: SPBC16A3_12c
 A: Map position: 2
 A: Introns: 11/2; 152/3; 282/1; 398/3
 C: Superfamily: triacylglycerol lipase, lingual

Query Match 22.5%; Score 505; DB 2; Length 443;
 Best Local Similarity 29.6%; Pred. No. 2.4e-36;
 Matches 125; Conservative 91; Mismatches 154; Indels 52; Gaps 13;

Qy 9 WIVSHRMEMW- LLIVAYMFORVNNSVHMPTKAVDPEAFNINSETIQHQYPCCEYEV A 66
 Db 35 YNIPERWENFVRYTLYLHYISSLTDGHTD -QKCNRIECEAFSYRVEHLVR 92

Qy 67 TEDGYTISLVRNRPGLVQPKT-GSREVVLQHGLVGASHWIS-NLPNNNLGFILADAG 124
 Db 93 TDQDNFLCLHRI---THPKQSOHKREVVYCHGLMTNSELSLWAVNESERSLPLIESG 148

Qy 125 FDWMMGNSRGNAWSRKHTLSIDDEWEWAFTSYDEMARFDUPAVINFLQKQGK1YYVG 184
 Db 149 YDWLGNRNGKNSRKHITYPKRDEEFWNFSTLDDMAMEFDIDTVDILREGREKINYIG 208

Qy 185 YSGTGTNGFLAFTSTMPMLAQIKMFALAPATVKHAKSPGTKELL--PDMMIKGFLGK 242
 Db 209 FSGTQAMALASINPDLNDKVNIFGLAPAYAPKGSFNSYFVDIYKVNPTIMYH-LFGR 267

Qy 243 KEPFLYQPRFLQVLYLQGQVLDQICSNIMMLGGFNTNNMSTASVYKAHTLAGTSV 302
 Db 268 RCLLPSVTFQN---ICYPFFVKIVDVSLSKILEWNDSLNSLNQKLCGFAHLSFSSV 323

Qy 303 ONLHNSOAVNSGELRAFD-----WGS-----TKNLERKCNQOPTPVYRVRDMT 346
 Db 324 KSVVHWLQIKNCTFQLYDDMALLAGYGSRHYQVPLFTNNI -KC----- 368

Qy 347 VPTAMWTFGGODLNSNPEDVKMILSEVNLNLYHKNIPERAWHDFINGLDAPHRMYNEIHL 406
 Db 369 -PMLIUNGKDTLINMVMYRMLPHAKEV--STAHYEHDLFLWQGDVKBEVFPVIDA 424

Qy 407 MQ 408
 Db 425 LK 426

RESULT 14

T31611 hypothetical protein Y50E8A.g - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C: Date: 29-Oct-1999
 C: sequence_revision 29-Oct-1999
 C: Accession: T31611
 R: Steward, C.
 A: Reference number: Z21047
 A: Accession: T31611
 A: Status: preliminary; translated from GB/EMBL/DBJ
 A: Molecule type: DNA
 C: Genetics:

A: Residues: 1-1585 <W11>
 A: Cross-references: EMBL:AL117200; NID:e1549770; PIDN:CAB55050_1; CESP:Y50E8A.g
 A: Introns: 25/3; 60/1; 133/2; 217/3; 337/2; 400/1; 746/2

Query Match 21.3%; Score 478.5; DB 2; Length 1585;
 Best Local Similarity 30.6%; Pred. No. 3.1e-33;
 Matches 118; Conservative 67; Mismatches 172; Indels 29; Gaps 9;

Qy 44 EAFMNISEIQHQYPCBEYEVATEDGYILSYNIRPQLVQPKKTG -SRPVVLLQHGLV 101
 Db 20 EETLDAADTISHYGYTVEKHYVTTDDGTVLQRIPIYGRDDRSILGCSKRPVVFFMHGLF 79

Qy	102 GGASNWISNLPPNNSLGPILADAGFDWGMNSRGNAWSRKHKTLSIDDEFAYFSYDEMAR 161	Qy	380 NIEPEWAHVDFING-----LDAPHMYNEITHLMMQQEETN 413
Db	80 GSSYHPLNLNPSSQAAITFADGFDWLGNTRGTEGLNHTSFSTINGVNENFSLEHSH 139	Db	409 KVSEYEHLDMINADTVKDYVPPVLRRLDIHHPEHEEND 449
Qy	162 FDLPAVINFILQKTKGQKIIYVGSQGTTMGMFIAFSTMPFL---AQKIKMYFALAPIAT 217		
Db	140 YDRRQEYVLDYQTRHESLFLYVGHQSCTA---VMFARLAEADVTWQSIRVFALGPTAG 196		
Qy	218 VKHAKSGOTKFLLPDMIKGKFLKQTRP---LRLQVITLGGQVILDQ 267		
Db	197 FMKPLMP---FVLEENVLYQALI---CFALDKFGFGLPVEIPRAIASKFADEFCSSKFTF 250		
Qy	268 ICSNIMLLGGFT-NNNNMSRASVYAAHTLQTSVONILHWSQAVNSGELRAFDGSET 326		
Db	251 LGSAGFVVAAGETLGQVNDSPKIPILSHFPTSATSTINLHWMQIYKHYEGRRLDGT-A 309		
Qy	327 KNELEKCNQOPTPYRVRDMTYPTAMNTGGDWLNSNPEDVKMLSEV-TNLIYHKNIPEW 384		
Db	31.0 RNLJAYSGQDAPRLEIGNIATQFLYFESKDDQITDEVRETIMKQMPGLJESYDLDHF 369		
Qy	395 ARVDFINGLDAHRYMEIILHMMQE 410		
Db	370 THEDFIGLRLRATEDVKPIVIRYKE 395		
RESULT 15			
T41053	triglyceride lipase-cholesterol esterase - fission yeast (Schizosaccharomyces pombe)		
C:Species:	Schizosaccharomyces pombe		
C:Date:	03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999		
C:Accession:	T41053		
R:Hilbert, H.; Duesterhoeft, A.; Wood, V.; Rajandream, M.A.; Barrell, B.G.			
Submitted to the EMBL Data Library, August 1998			
A:Reference number:	221967		
A:Accession:	T41053		
A:Status:	preliminary; translated from GB/EMBL/DBJ		
A:Molecule type:	DNA		
A:Residues:	1-467 <HIL>		
A:Cross references:	EMBL:AU031324; PIDN:CAA2047.1; GSPDB:GN000668; SPDB:SPCC1672.09		
A:Experimental source:	strain 972h-; cosmid c1672		
C:Genetics:			
A:Gene:	SPDB:SPCC1672.09		
A:Map position:	3		
A:Introns:	12/2; 164/3; 294/1		
RESULT 16			
Query Match	21.1%	Score 475;	DB 2;
Best Local Similarity	31.28;	Prd. No. 1.1e-33;	Length 467;
Matches	125;	Conservative	68; Mismatches 158; Indels 50; Gaps 12;
Qy	39 KAVDPEAFMNISEIIQHOGYPCDEYEWATEDGYILSWNRIP-----GLVQPKKTGSRP 92		
Db	73 KAIHDAA---DIREMCKISGYYWEDHLYRTEDDYILCTHRISKDSPGRIGSPHPKKL--P 127		
Qy	93 VVLLQHGLYGGASNWISNL-PNNNSLIGTADAGFDWGMNSGRGNAWSRKHKTLSIDDEF 151		
Db	128 VYUCHHGSLMNSEVWVNVDPNCNLFLYFLVNGYDWTWGNRNGNKYXSRHQLRFDSTKEF 187		
Qy	152 WAFSYDEMARFDLPAVINFILQKTKGQKIIYVGSQGTTMGMFIAFSTMPFLAOKIMYFA 211		
Db	188 WDESIDFQAQDIPDTDYLKTSQKLTYIGFSQQTAAQAFASLSSHPLNDKINSLIA 247		
Qy	212 LAPIATYKHAKSPGTKEFLPMMIG-----LGKKEKLYQTRFLRQVLYLGQVVI 264		
Db	24.8 LAP-----AISPKGLNRLNRPVDAFKARPSLFLFRKSLTPSAGFWQSFH---APKF 297		
Qy	265 LDOICSNIMLLGGFTNNNNMSRASVYAAHTLQTSVONILHWSQAVNSGELRAFD--- 321		
Db	298 EDVLAYCQLSQLFNWSQNSISSIONYFALSYVSKCLVHWFQIMRSAREFRMDNDQ 357		
Qy	322 WGE-----TKNLERKNOPPVPVYRVRDMWVPTAMWTGGDWLSNPEDYKMLSEVTNLHYK 379		
Db	358 LGHDYFLKYYKAFAKFP-----NNNTPFLWGGDSL---VDIQAMLNALPAEVH 408		

Result No.	Score	Query	Match	Length	DB	ID	Description
1	1289		399	1	LICH_HUMAN	P38871	homo sapien
2	1220.5	54.3	397	1	LICH_RAT	Q61194	rattus norvegicus
3	1197.5	53.3	397	1	LICH_MOUSE	Q9zdm5	mus musculus
4	1164.5	51.8	395	1	LIGP_RAT	P04634	rattus norvegicus
5	1154	51.4	398	1	LIGP_CANFA	P80035	canis familiaris
6	1139	50.7	397	1	LIGP_BOVIN	Q2958	bos taurus
7	1119	49.8	398	1	LIGP_HUMAN	P07098	homo sapiens
8	663	29.5	394	1	LIP3_DROME	Q46108	drosophila
9	546	24.3	439	1	LIP1_DROME	Q46107	drosophila
10	422.5	18.8	548	1	TGL1_YEAST	P34163	saaccharomyces cerevisiae
11	126	5.6	987	1	YD94_METJA	Q58789	methanococcus
12	105	4.7	430	1	ORC2_CAEEL	Q21037	caenorhabditis elegans
13	101	4.5	436	1	PT1P_SALTY	P70683	c platelet
14	96.5	4.3	287	1	Y193_HAEIN	Q57427	haemophilus ducreyi
15	95.5	4.3	1259	1	LIN1_HUMAN	P08547	homo sapiens
16	93.5	4.2	277	1	PRXC_STRAU	Q31168	streptomyces
17	93	4.1	569	1	PTRD_PLAFA	Q8910	plasmid
18	92	4.1	748	1	PT1P_ECOLI	P37177	escherichia coli
19	92	4.1	748	1	PT1P_SALTY	P37178	salmonella
20	91	4.0	370	1	P2C2_SCHPO	Q09172	schizosaccharomyces pombe
21	90.5	4.0	1037	1	ACRD_ECOLI	P24177	escherichia coli
22	90	4.0	277	1	BPA2_STRAU	P29715	streptomyces
23	90	4.0	1122	1	YGC3C_YEAST	P53280	saaccharomyces cerevisiae
24	90	4.0	1136	1	POLG_MMV	P2034	caenorhabditis elegans
25	90	4.0	2083	1	DYSF_MOUSE	Q9e8d7	mus musculus
26	89	4.0	330	1	EXO4A_RHIME	P33691	rhizobium m
27	88.5	3.9	185	1	YCHB_BACSU	Q31482	bacillus subtilis
28	88.5	3.9	869	1	CFAC_ECOLI	P25733	escherichia coli
29	87	3.9	473	1	SCRB_LACLA	Q04937	lactococcus
30	86.5	3.8	382	1	YDH4_HAEIN	P44861	haemophilus ducreyi
32	86.5	3.8	685	1	INVA_SALTY	P35657	salmonella
33	86	3.8	1882	1	Y468_MYCPN	P75109	mycoplasma
			525	1	ACU8_NEUCCR	P15937	neurospora crassa

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt; 40.47

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1							
LICH_HUMAN		STANDARD;		PRT;		399 AA.	
ID	Q16529; Q36EJ0;	AC	P3851; Q16529; Q36EJ0;	DT	01-OCT-1994 (Rel. 30, Created)	DT	01-OCT-1994 (Rel. 30, Last sequence update)
						DE	Lysosomal acid lipase/cholesterol ester hydrolase precursor (EC 3.1.1.13) (LAL) (Acid cholestry ester hydrolase) (Sterol esterase) (Lipase A) (Cholestry esterase).
LNPA						DN	
OS	Homo sapiens (Human).					NCBI_TaxID:9606;	
RN						SEQUENCE FROM N.A., AND SEQUENCE OF 1996-212; 277-297 AND 305-315.	
RX						MEDLINE:92042192; PubMed=1718995;	
RA	Anderson R.A., Sando G.N.;					"Cloning and expression of cDNA encoding human lysosomal acid lipase/cholesterol ester hydrolase. Similarities to gastric and lingual lipases."	
RT						RT	
RT						RL	J. Biol. Chem. 266:22479-22484(1991).
RT						RN	
RT						SEQUENCE FROM N.A.	
RT						RC	SEQUENCE FROM LIVER;
RT						RX	MEDLINE:9415897; PubMed=8112342;
RA	Amels D., Merkx M., Eckerstor C., Greten H.;					RA	"Purification, characterization and molecular cloning of human hepatic lysosomal acid lipase."
RT						RT	Eur. J. Biochem. 219:905-914(1994).
RL						RN	
RN						SEQUENCE FROM N.A.	
RC						RC	SEQUENCE FROM LIVER;
RX						RX	MEDLINE:9636357; PubMed=8725147;
RA	Du H., Witte D.P., Grabowski G.A.;					RA	"Tissue and cellular specific expression of murine lysosomal acid lipase mRNA and protein."
RT						RT	Proc. Natl. Acad. Sci. U.S.A. 91:2718-2722(1994).
RL						RN	
RN						RN	SEQUENCE FROM N.A.
RC						RC	SEQUENCE FROM Placenta;
RA						RA	Strasbourg R.;
RT						RT	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RL						RL	
RN						RN	VARIANT CESD/HD PRO-200.
RP						RX	MEDLINE:9419514; PubMed=8146180;
RA	Anderson R.A., Byrum R.S., Coates P.M., Sando G.N.;					RA	"Mutations at the lysosomal acid cholestry ester hydrolase gene locus in Wolman disease."
RT						RT	Proc. Natl. Acad. Sci. U.S.A. 91:2718-2722(1994).
RL						RN	
[6]						RN	VARIANT CESD/HD PRO-129 AND PRO-129.
RP						RX	MEDLINE:98295576; PubMed=9633819;
RA	Ries S., Buechler C., Schindler G., Aslanidis C., Amets D., Gasche C.,					RA	"Tissue and cellular specific expression of murine lysosomal acid lipase mRNA and protein."
Jung N., Schambach A., Fehringen P., Vanier M.T., Belli D.C.,						RA	

RA	Greten H., Schmitz G.;	Score 1289; DB 1; Length 399;
RT	"Different missense mutations in histidine-108 of lysosomal acid esterases cause cholesterol ester storage disease in unrelated compound heterozygous and hemizygous individuals."	;
RT	Hum. Mutat. 12:44-51(1998).	;
RL	-1- FUNCTION: CRUCIAL FOR THE INTRACELLULAR HYDROLYSIS OF CHOLESTERYL ESTERS AND TRIGLYCERIDES THAT HAVE BEEN INTERNALIZED VIA RECEPTOR-MEDIATED ENDOCYTOSIS OF LIPOPROTEIN PARTICLES. IMPORTANT IN MEDIATING THE EFFECT OF LDL (LOW DENSITY LIPOPROTEIN) UPTAKE ON SUPPRESSION OF HYDROXYMETHYLGLUTARYL-COA REDUCTASE AND ACTIVATION OF ENDOGENOUS CELLULAR CHOLESTERYL ESTER FORMATION.	;
CC	-1- CATALYTIC ACTIVITY: A sterol ester + H(2)O = a sterol + a fatty acid.	;
CC	-1- SUBCELLULAR LOCATION: Lysosomal. DEFECTS IN LIPA ARE THE CAUSE OF THE SEVERE INFANTILE-ONSET WOLMAN DISEASE (WD) AND THE MILD LATE-ONSET CHOLESTERYL ESTER STORAGE DISEASE (CESD).	;
CC	-1- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY.	;
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	;
CC	EMBL; M74775; AAA59519.1; -	;
DR	DR EMBL; U04285; AABE0327.1; -	;
DR	DR EMBL; U04286; AABE0327.1; JOINED.	;
DR	DR EMBL; U04287; AABE0327.1; JOINED.	;
DR	DR EMBL; U04288; AABE0327.1; JOINED.	;
DR	DR EMBL; U04290; AABE0327.1; JOINED.	;
DR	DR EMBL; U04291; AABE0327.1; JOINED.	;
DR	DR EMBL; U04292; AABE0327.1; JOINED.	;
DR	DR EMBL; U04293; AABE0327.1; JOINED.	;
DR	DR EMBL; X76488; CAA54026.1; -	;
DR	DR EMBL; U08464; AABE0328.1; -	;
DR	DR EMBL; BC012287; AABE0328.1; -	;
PIR	PIR: A39315; A39315.	;
DR	DR InterPro; IPR000073; Abhydrolase.	;
DR	DR InterPro; IPR000734; Lipase.	;
DR	DR PROSITE; PS00120; LIPASE_SER; 1.	;
KW	KW Hydrolase; Lipid degradation; Glycoprotein; Signal; Lysosome;	;
KW	KW Disease mutation; Polymorphism.	;
FT	FT SIGNAL 1 21	POTENTIAL.
FT	FT CHAIN 22 399	LYSOSOMAL ACID LIPASE/CHOLESTERYL ESTER HYDROLASE.
FT	ACT_SITE 174 174	CHARGE RELAY SYSTEM. (BY SIMILARITY).
FT	ACT_SITE 374 374	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	CARBOHYD 36 36	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD 72 72	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD 101 101	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD 161 161	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD 273 273	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD 321 321	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	VARIANT 16 16	P -> T.
FT	VARIANT .129 .129	H -> P (IN CESD).
FT	VARIANT .129 .129	/FTid=VAR_004248.
FT	VARIANT 200 200	H -> R (IN CESD).
FT	VARIANT 29 29	/FTid=VAR_004249.
FT	CONFICT 23 23	L -> P (IN CESD AND WD).
FT	CONFICT 29 29	/FTid=VAR_004250.
FT	SEQUENCE 399 AA; 399 AA;	G -> R (IN REF. 3).
CC	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way	;
CC	CC -1- CATALYTIC ACTIVITY: A sterol ester + H(2)O = a sterol + a fatty acid.	;
CC	CC -1- SUBCELLULAR LOCATION: Lysosomal. BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.	;
CC	CC -1- SIMILARITY: BELOWS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.	;
CC	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way	;

modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.lsб-sib.ch/announce/> or send an email to licensed@lsб-sib.ch).

CC STRAIN=C57BL/6 X CBA; TISSUE=Liver;
 CC MEDLINE=93363957; PubMed=8725147;
 CC RA DR H., Witte D.P., Grabowski G.A.;
 CC RT "Tissue and cellular specific expression of murine lysosomal acid
 CC RT lipase mRNA and protein.";
 CC RT Lipid Res. 37:937-949(1996).
 CC -I- FUNCTION: CRUCIAL FOR THE INTRACELLULAR HYDROLYSIS OF CHOLESTERYL
 CC ESTERS AND TRIGLYCERIDES THAT HAVE BEEN INTERNALIZED VIA RECEPTOR-
 CC -I- PROTEIN. IMPORTANT IN
 CC MEDiated ENDOCYTOSIS OF LIPOPROTEIN PARTICLES. IMPORTANT IN
 CC MEDiating THE EFFECT OF LDL (LOW DENSITY LIPOPROTEIN) UPTAKE ON
 CC SUPPRESSION OF HYDROXYMETHYLGLUTARYL-COA REDUCTASE AND ACTIVATION
 CC OF ENDOGENOUS CELLULAR CHOLESTERYL ESTER FORMATION (BY
 CC SIMILARITY).
 CC -I- CATALYTIC ACTIVITY: A sterol ester + H₂O = a sterol + a fatty
 CC acid.
 CC -I- SUBCELLULAR LOCATION: Lysosomal.
 CC -I- TISSUE SPECIFICITY: Expressed at low levels in most tissues. High
 CC level expression is found in hepatocytes and splenic and thymic
 CC cells. Very high level expression is observed in cells of the
 CC small intestinal villi, the zona fasciculata and reticularis of
 CC the adrenal cortex, pancreatic acini, and renal tubular
 CC epithelium.
 CC -I- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.
 CC -I- This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.lsб-sib.ch/announce/>
 CC or send an email to licensed@lsб-sib.ch).
 CC -I-
 EMBL: 231659; CA83494.1; -.
 DR MGI: 967789; LipI.
 DR InterPro: IPR000073; Abhydrolase.
 DR InterPro: IPR000734; Lipase.
 DR InterPro: IPR000379; Ser.estr.site.
 DR Pfam: PF00561; abhydrolase; 1.
 DR PROTEIN: PS00120; LIPASE_SBR; 1.
 DR HYDROLASE; Lipid degradation; Glycoprotein; Signal; Lysosome.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 397 HYDROLASE.
 FT ACT_SITE 172 172 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 372 372 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 99 99 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 271 271 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 319 319 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SEQUENCE 397 AA: 45186 MW: 9738593A023947 CRC64;
 SQ 397 PT--KAVDPFAFMSETIQQHGPCEEEYATEDGYIILSVNRPGLVQPKTKTGSRPV 93
 PT 20 PTGTISAVDPFAAMNVTETIMHWGP--EHSVQTGDDYIIGVHPIPHGKKNQFDKGPKpV 77
 SEQUENCE 397
 Query Match 54.3%; Score 1220.5%; DB 1; Length 397;
 Best Local Similarity 58.2%; Prid. No. 2.5e-98;
 Matches 220; Conservative 67; Mismatches 84; Indels 7; Gaps 3;
 Qy 152 WAFSDDEMARDLPAVINFQKTKQEKIYVGVSQGTMGFIASFSTMPLEAQIKIMYFA 211
 Db 138 WAFSDDEMAYDLPASINVYLNKNGEQEQLYNGHISQGCTGTGFIASFQMFELAKVYMFPA 197
 Qy 212 LAPIATVKAHKSPGTKFLLPDMIKLGFKKEFLYQTRFLRQVLYLGQVILDQICSN 271
 Db 198 LAPVLSLNFAFGPVMKLRPLDLEDFGQKQFLPQSMVQKWLSTHICHTVINKELCAN 257
 Qy 272 IMLLGGENTNNMAMSASYAATLQASVQNTLHWSDAVNSGLRAFDWGSETKLEK 331
 Db 258 IFFLIGFENPKNLNNRNRVDDYTHPAGTQSVQNNHWTQVYKIRQADPDWGSDDKANYFH 317
 Qy 332 CNOQPTPVRVYRDMTPTAMWGGDQLSNPDEVYKMLLSEVTNLYHKNIPEWAHYDFIW 391
 Db 318 YNQSYSPPLYSIKDQMLPTALWSSGRDWLADTS DINLLEIPTIYVHKNIPENDHDFIW 377
 Qy 392 GLDAPHRMYNEIIHMQQ 409
 Db 378 GLDAPWRYNEVVSLLMK 395
 Query Match 53.3%; Score 1197.5%; DB 1; Length 397;
 Best Local Similarity 55.6%; Prid. No. 2.5e-96;
 Matches 217; Conservative 70; Mismatches 100; Indels 3; Gaps 1;
 Qy 23 VAYMFQRNVNSVHMPF--KAVDPFAFMSETIQQHGPCEEEYATEDGYIILSVNRPV 79
 Db 6 LFEVFTIGILSRVPVGTYSADPVEYNMNTTEIMWGPGEHSVLTGDIYLTHRIP 65
 Qy 80 RGLVQPKTGTGSPRVVLLQHGLVGGASRNWISNLPNSLGFILADAGFDWGNNSRGNAWSR 139
 Db 66 RGWKNHFGKGPVPLQHGLADSNWVINDNSLGFILADRGFDWAGNSRGNTWLS 125
 Qy 140 KFKTLISDQDEFWASYDEMARFDLPAVINFQKTKQEKIYVGVSQGTMGFIASFSTM 199
 Db 126 KFKTLISDQDEFWASYDEMARFDLPAVINFQKTKQEKIYVGVSQGTMGFIASFQSM 185
 Qy 200 PELAKKIKMFLAPLAVTKRKAQSPGKTFLLPDMIKLGFKKEFLYQTRFLRQVLYL 259
 Db 186 PELAKKIKMFLAPLAVSLNFAFGPVMKLRPLDLEDFGQKQFLPQSMVQKWLSTH 245
 RN 11
 RP SEQUENCE FROM N.A.

RESULT 3

LICH_MOUSE

STANDARD; PRT; 397 AA.

Qy 23 VAYMFQRNVNSVHMPF--KAVDPFAFMSETIQQHGPCEEEYATEDGYIILSVNRPV 79
 Db 6 LFEVFTIGILSRVPVGTYSADPVEYNMNTTEIMWGPGEHSVLTGDIYLTHRIP 65
 Qy 80 RGLVQPKTGTGSPRVVLLQHGLVGGASRNWISNLPNSLGFILADAGFDWGNNSRGNAWSR 139
 Db 66 RGWKNHFGKGPVPLQHGLADSNWVINDNSLGFILADRGFDWAGNSRGNTWLS 125
 Qy 140 KFKTLISDQDEFWASYDEMARFDLPAVINFQKTKQEKIYVGVSQGTMGFIASFSTM 199
 Db 126 KFKTLISDQDEFWASYDEMARFDLPAVINFQKTKQEKIYVGVSQGTMGFIASFQSM 185
 Qy 200 PELAKKIKMFLAPLAVTKRKAQSPGKTFLLPDMIKLGFKKEFLYQTRFLRQVLYL 259
 Db 186 PELAKKIKMFLAPLAVSLNFAFGPVMKLRPLDLEDFGQKQFLPQSMVQKWLSTH 245
 RN 11
 RP SEQUENCE FROM N.A.Qy 23 VAYMFQRNVNSVHMPF--KAVDPFAFMSETIQQHGPCEEEYATEDGYIILSVNRPV 79
 Db 6 LFEVFTIGILSRVPVGTYSADPVEYNMNTTEIMWGPGEHSVLTGDIYLTHRIP 65
 Qy 80 RGLVQPKTGTGSPRVVLLQHGLVGGASRNWISNLPNSLGFILADAGFDWGNNSRGNAWSR 139
 Db 66 RGWKNHFGKGPVPLQHGLADSNWVINDNSLGFILADRGFDWAGNSRGNTWLS 125
 Qy 140 KFKTLISDQDEFWASYDEMARFDLPAVINFQKTKQEKIYVGVSQGTMGFIASFSTM 199
 Db 126 KFKTLISDQDEFWASYDEMARFDLPAVINFQKTKQEKIYVGVSQGTMGFIASFQSM 185
 Qy 200 PELAKKIKMFLAPLAVTKRKAQSPGKTFLLPDMIKLGFKKEFLYQTRFLRQVLYL 259
 Db 186 PELAKKIKMFLAPLAVSLNFAFGPVMKLRPLDLEDFGQKQFLPQSMVQKWLSTH 245
 RN 11
 RP SEQUENCE FROM N.A.Qy 23 VAYMFQRNVNSVHMPF--KAVDPFAFMSETIQQHGPCEEEYATEDGYIILSVNRPV 79
 Db 6 LFEVFTIGILSRVPVGTYSADPVEYNMNTTEIMWGPGEHSVLTGDIYLTHRIP 65
 Qy 80 RGLVQPKTGTGSPRVVLLQHGLVGGASRNWISNLPNSLGFILADAGFDWGNNSRGNAWSR 139
 Db 66 RGWKNHFGKGPVPLQHGLADSNWVINDNSLGFILADRGFDWAGNSRGNTWLS 125
 Qy 140 KFKTLISDQDEFWASYDEMARFDLPAVINFQKTKQEKIYVGVSQGTMGFIASFSTM 199
 Db 126 KFKTLISDQDEFWASYDEMARFDLPAVINFQKTKQEKIYVGVSQGTMGFIASFQSM 185
 Qy 200 PELAKKIKMFLAPLAVTKRKAQSPGKTFLLPDMIKLGFKKEFLYQTRFLRQVLYL 259
 Db 186 PELAKKIKMFLAPLAVSLNFAFGPVMKLRPLDLEDFGQKQFLPQSMVQKWLSTH 245
 RN 11
 RP SEQUENCE FROM N.A.

DR	PF00561; abhydrolase; 1.
DR	PROSITE; PS00120; LIPASE_SER; 1.
RW	Hydrolase; Lipid degradation; Glycoprotein; Signal.
FT	SIGNAL 1 19
FT	CHAIN 20 398 TRACYGLYCEROL LIPASE, GASTRIC.
FT	ACT-SITE 172 172 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	ACT-SITE 372 372 N LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBONYD 34 34 N LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBONYD 99 99 N LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBONYD 271 271 N LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBONYD 327 327 N LINKED (GLCNAC. .) (POTENTIAL).
FT	CONFLICT 39 39 I > T (IN REF 39) Ser-esters-site.
SQ	SEQUENCE 398 AA; 45130 MW; E04D62F7518E386C CRC64;
Query Match	51.4%; Score 1154; DB 1; Length 398;
Best Local Similarity	54.3%; Pred. No. 1.5e-92;
Matches	216; Conservative 71; Mismatches 99; Indels 12; Gaps 5;
Qy	17 MWLLILVAYMFORVNVSН-----MPTKAVDPEAFMNISETIOHOGCPEBEYATEDG 70
Db	1 MWLLPAASVTS-TLGTGTHDEFGKLHPT--NPEVNMNISMITYWGPAEYEVTEDG 56
Qy	71 YILSVNRIPRGLVQPKTGSRPVVLQHGLVGASWMSNLPNSLGGFILADAGEDWMG 130
Db	57 YLGIDIPYGRKNSNIGRREPVALQHGLASATWNISLPNSNPAFLADAGDyDWLG 116
Qy	131 NSRGNAWSRKHTLSIDQDETFWASDYMEDPDLPAVINFLQTKQEKIYVGTSQGT 190
Db	117 NSRGNTWARRNLYYSPPSVWEAFSPEMAYKDLPAIDFLIKKTCQDKLHYVGHSQTT 176
Qy	191 NGFTIASTMPMELAQKIKMVFALAPIATVKHAKSPGTKFLLPDMMIKGFLGKKEFLYQTR 250
Db	177 TGPIAFTNPKIAKRINTFYAIAPVAVTKYETILLNKLMLYPSFLKRIPNKF-YPHH 235
Qy	251 FLRQ-LVYLQGQVILQDQICNSIMLIGGENTNNMMSRASYAAHTLAGTSVQNLHWS 309
Db	236 FFDQFLATEVCSTREVLCLCSNALFTGFDTMNLRSLDYLTSHPAGTSVQNLHWS 295
Qy	310 QAVNSGLRAFDGSETKNLNCNQTPPPVVRDWTMVTQPAWQDQDWLSNPEDYKML 369
Db	296 QAVKSGRFOAFDGSPPQNMMHYHQSKPPYNLTDHPIAVWNGNDLLADPHYDYL 355
Qy	370 SEVTNLHYKNPEAHVDFTWGLDAFPHYMEIILHM 407
Db	356 SKLPNLHYKRKIPPNNLDFIWAMDAFQAVINEIVSPM 393
RESULT 6	
LIPG_BOVIN	STANDARD; PRT; 397 AA.
ID	
AC	Q9458;
DT	30-MAY-2000 (Rel. 39, Created)
DT	30-MAY-2000 (Rel. 39, Last sequence update)
DT	15-JUN-2002 (Rel. 41, Last annotation update)
DE	Triacylglycerol lipase, pregastric precursor (EC 3.1.1.3) (Pregastric lipase) (GL) (Pregastric esterase) (PGE).
GN	LIPF.
OS	Bos taurus (Bovine).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC	Bovidae; Bovinae; Bos.
OX	NCBI_TaxID=9913;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE-Tongue serous gland;
RC	LINE-9501625; Pubmed=7926811;
RA	Thümmermans M.Y.J., Kuipers L.P., Teuchy H.;
RT	"The cDNA sequence encoding bovine pregastric esterase."
RL	Gene 14:259-262(1994)
CC	-1 - CATALYTIC ACTIVITY: Triacylglycerol + H ₂ O = diacylglycerol + a fatty acid anion.
CC	-1 - SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.
CC	[1]
SEQUENC: FROM N.A.	
RESIDUE 7	
LIPG_HUMAN	STANDARD;
ID	LIPG_HUMAN
AC	P07098;
DT	01-APR-1988 (Rel. 07, Created)
DT	15-JUN-2002 (Rel. 41, Last sequence update)
DE	Triacylglycerol lipase (GL).
GN	LIPF.
OS	Homo sapiens (Human).
OC	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Eutheria; Primates; Catarrhini; Homidae; Homo.
NCBI_TaxID=9606;	
RN	[1]

RESULT 11	YD94_METJA	STANDARD;	PRT;	987 AA.	QY	300 TSVQNL-HWSQAVNSGELRAFMGSETKNLEKCNQOPTPVR--YRVRDMTVPTAMWTGGQ 356
AC	Q58189;				Db	633 TLFENVLGNSYSSERDNLILAKYGPALKIENYNGTNTNTS1KGWYASGTS1S1STDHGTG 692
DT	15-JUL-1998 (Rel. 36, Created)				QY	357 --DWLSN---PDEVKMLLSEVTNL1YHKNIPENA 385
DT	15-JUL-1998 (Rel. 36, Last sequence update)				Db	693 INWIENTFKNDAKSYSFNLNL---NI--NA 720
DE	Hypothetical protein MJ1394.					
GN	Methanococcus jannaschii					
OS	Archaea; Euryarchaeota; Methanococci; Methanococcales;					
OC	Methanococcaceae; Methanococcaceae.					
OX	NCBI_TAXID=2190;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN-JAL-1 / DSM 2661 / ATCC 43067;					
RX	MEDLINE-96337999; PubMed-8688087;				AC	021037; 35, Created
RA	Bell C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D., Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I., Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C., RT				DT	01-NOV-1997 (Rel. 36, Last sequence update)
RA	"Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii";				DT	15-JUN-2002 (Rel. 41, Last annotation update)
RA	Science 273:1058-1073(1996).				DE	Origin recognition complex subunit 2 (CeOrc2).
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).				GN	ORC-2 OR F59E10.1.
CC	-1- SIMILARITY: TO M.JANNASCHII MJ1393 AND A.FUGIDUS AF2028.				OS	Caenorhabditis elegans..
CC	-				OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Rhabditidae; Caenorhabditis.
CC	-				OC	Rhabditidae; Peledorinae; Caenorhabditis.
CC	-				NCBI_TaxID=6219;	
CC	-				RN	[1]
CC	-				RP	SEQUENCE FROM N.A.
CC	-				RX	MEDLINE-96099401; PubMed-7502077;
CC	-				RA	Gavin K.A., Hidaka M., Stillman B.;
CC	-				RT	"Conserved initiator proteins in eukaryotes. ";
CC	-				RL	Science 270:1667-1671(1995).
CC	-				RN	[2]
CC	-				RP	SEQUENCE FROM N.A.
CC	-				RC	STRAIN-Bristol N.
CC	-				RA	Swinburne J.;
CC	-				RL	Submitted (AUG-1994) to the EMBL/GenBank/DDJB databases.
CC	-				RN	[3]
CC	-				RP	REVISIONS.
CC	-				RA	Jones S.J.M. /
CC	-				RA	Submitted (MAR-1997) to the EMBL/GenBank/DDJB databases.
CC	-				CC	-1- FUNCTION: COMPONENT OF THE ORIGIN RECOGNITION COMPLEX (ORC) THAT BINDS ORIGINS OF REPLICATION. IT HAS A ROLE IN BOTH CHROMOSOMAL REPLICATION AND MATING TYPE TRANSCRIPTIONAL SILENCING. BINDS TO THE ARS CONSENSUS SEQUENCE (ACS) OF ORIGINS OF REPLICATION IN AN ATP-DEPENDENT MANNER.
CC	-				CC	-1- SUBUNIT: ORC IS COMPOSED OF SIX SUBUNITS (BY SIMILARITY).
CC	-				CC	-1- SUBCELLULAR LOCATION: NUCLEAR.
CC	-				CC	-1- SIMILARITY: BELONGS TO THE ORC2 FAMILY.
DR	U67579; AAB99404.1; -				CC	-
DR	TIGR: MJ1394; -				CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
FT	TRANSMEM				CC	-
FT	TRANSMEM	12	32	POTENTIAL.	CC	-
FT	TRANSMEM	958	978	POTENTIAL.	CC	-
SQ	SEQUENCE	987 AA;	112360 MW;	DIE628FB28A86D CRC64;	CC	-
DR	EMBL; U67579; AAB99404.1; -				DR	EMBL: U40270; AAC46954.1; -
DR	TIGR: MJ1394; -				DR	EMBL: Z36549; CAR85415.1; -
KW	Hypothetical protein; Transmembrane; Complete proteome.				DR	WormDB; F59E10.1; CE11692.
QY	3 ETLSRQWYSHMRMFLWLLIVAYMFDQ--NVRSHMPTKAVDEAFN--			48	KW	DNA replication; Nuclear protein.
Db	340 ETYDVKIPANKMSEWVNLLVNLKVNLYPGENVNVNVIKYLNSNGQFYDNFENWTGWQ 399				SQ	SEQUENCE 430 AA; 49319 MW; 54FC086BB4AD9670 CRC64;
QY	49 --.-ISETLHQG-YQPEEYEVATEDGYIISVNRIPRG--LYQPKRTGSREVVLQH 98					
Db	400 YKNGIVQWSISQISQISLEYKIST--S1NDPQNGYKLLPQGK RDVVI--S 450					
QY	99 GLVGGASNNISNLPNLPSLGFILDAFGDYMGNRSRKHKT--LSIDQ-----148					
Db	451 GWWYRPSNW GGGPDRIG -LEDENFD-----GYSPEVNHYSNISIDRRTNGNPB 500					
QY	149 --DEFWAFSYDEMAREFLDIAVINEFLQKIGQKIIYVQYSQGTTMGIATFNSMPLEAQK 205					
Db	501 ISPEYWNPPEDNEYXFEL-----K1-----YSNGT-----ITFST-----531					
QY	206 IKMYPALAPI-ATYKHAKSPGTKF-----LLPDMIKG---LGKKEFLYQTR 250					
Db	532 --YQNGSLANTVSTDITYTKDRVVKHGGYVYDLEVNSKNEFPYGDRAWKYL-- 586					
QY	251 FLRQLVYIYLQGQVILQICSNMILLGG-----FNTNNNMNSRASVYAAHTL---AG 299					
Db	587 -----EITSANSEGATVFLGDFYFKDQYDFTKCDLPLRNYYTKDNTFEFK 138					

CC or send an email to license@ib-sib.ch).

CC

DR EMBL: U32704; AAC21862.1; -.

DR TIGR: H10193; -.

DR InterPro; IPR00073; Abhydrolase.

DR InterPro; IPR00319; Ser-esters-site.

DR Pfam: PF00561; abhydrolase; 1.

KW Hypothetical protein; hydrolase; Serine esterase; Complete proteome.

FT ACT SITE 119 119 BY SIMILARITY.

FT ACT SITE 266 266 BY SIMILARITY.

SQ SEQUENCE 287 AA; 32987 MW; FB548619C060619 CRC64;

Query Match Score 96.5; DB 1; Length 287;

Best Local Similarity 19.1%; Pred. No. 0.53; Gaps 12;

Matches 62; Conservative 39; Mismatches 119; Indels 105; Gaps 12;

Qy 84 QPKKTGSRPVVULLQHGLGGASWNISNLPNNSLGFFILADAGFDVWGNRSRGNAWSRKHKT 143

Db 39 QVKOTRINTPVVPLIFHGFMDN-----LGVI-----ARAFSEHYSI 75

Qy 144 LSIDQDEWFAFSIDEMARFDLPAV- INFILQTKQEIYVYQSYQGTGFMFTAFTSNEPEL 202

Db 76 LRIDLRNIGHSPFSEKMYQLMEDVAVIRHNLNSKVYLIGHSMGGKTAMKITALCPEL 135

Qy 203 AQKIKMYFALAPIATVHAKSPGTKFLLPDM-----MIKGLEFGKKEFLYQTR 250

Db 136 VEK-----LIVIDNSPMPTEGGHHDVFGHLDVFGNLFAVYNAKEN- 171

Qy 251 FLRQLVIVLGQVYLDQICSNIMLIGGFTNTNNMMSRASVYAAHTLAGTSVONILHWSQ 310

Db 172 -RQQAQPKILOEINDE-DVVOQFLMKSFDVNSADCPEFNL---TALFNNYANTMOWE- 222

Qy 311 AVNSGEGLRAFDWGSBTKNLEKCHQPTPRYRVDMTVGGQWLSNPDVDMV 370

Qy 371 EVTNLHYH-KNIPEWAHY---DFI 390

Db 223 -----KVRYF-----TPTLF1KGNNSSYK1ENSEKILE 251

Qy 252 QFPNATRAFTINGSHWAEKPDEV 276

RESULT 15

LIN1_HUMAN STANDARD PRT: 1259 AA.

ID LIN1_HUMAN

AC P08577;

DT 01-AUG-1988 (Rel. 08, Created)

DT 01-AUG-1988 (Rel. 08, Last sequence update)

DT 01-AUG-1988 (Rel. 08, Last annotation update)

DE LINE-1 reverse transcriptase homolog.

OS Homo sapiens (Human).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

RN [1]

RP SEQUENCE.

RX MEDLINE=66230917; PubMed=2423883;

RA Hattori M.; Kubara S.; Takehara O.; Sakai Y.;

RT "L1 family of repetitive DNA sequences in primates may be derived from a sequence encoding a reverse transcriptase-related protein.";

RL Nature 321:625-628(1986).

CC -I - MISCELLANEOUS: THIS SEQUENCE WAS CONSTRUCTED FROM AN ALIGNMENT OF PUBLISHED AND UNPUBLISHED SEQUENCES, DETERMINED IN VARIOUS LABORATORIES, BELONGING TO THE LINE-1 FAMILY.

CC PIR: A25313; GNHULL.

DR InterPro; IPR005135; Exo_endo_phos.

DR InterPro; IPR00300; IPPC.

DR InterPro; IPR00477; RVTS.

DR Pfam: PF00078; rvt; 1.

DR SMART; PF0372; Exo_endo_phos; 1.

DR SMRT; SM00128; IPPC; 1.

KW RNA-directed DNA polymerase.

SQ SEQUENCE 1259 AA; 147112 MW; F3BC18A3803919F5 CRC64;

Query Match Score 4.3%; Best Local Similarity 19.7%; Matches 90; Conservative 67; Mismatches 170; Indels 129; Gaps 23;

Qy 28 QRNNVSUHMPTKAVDPEAFMNI---SETIQHQYPCCEEYE-----

Db 442 QEEVESLNRPITSEEAIIINSLPNKKSPGPBEGFTAEFYQRYKEELVPFLLKUQFQSIEKE 501

Qy 65 -VTEDGILSVRIPR GLYQVKKTGERPVVL-----LQGLVGGASNWNSL-PNN 114

Db 502 GIIPNSFVEASILIPKGRDTTKENPRPISMNIDAKILNWLANOIQHHKKLIIHD 501

Qy 115 SFGFILADAGFDVWMGNSR-----GNAWSRKHKTLSIDQDEFWAFSYDEM----- 159

Qy 160 -----ARFDLPAVINFLQKTOEKEIYVGSQGTTMGFIASPTMPLEA 203

Db 615 PUNKLGIDGTYLKIRALYDKPTA-NIIL-NSQ-KLEAPPLKTGRQGCPSPPLPNIV 670

Qy 204 QKTKMYFAJAPATVHAKSPGTKFLLPDMMIKLGFKEFYQTRFLYLGCGV 263

Db 671 LEV-----LA- FAIRQEKE-----IKGIQLGKEEKFLSLEADDMIVYLENPI 711

Qy 264 ILDQICSNIMLILGGFN-----TNNNMMSRASYTAAHTLAGTSVONILHWSQAVNSGELR 318

Db 712 VSQ---NELLKLSNFNSKVSGYIINVQKSQAFYTNNROTESQIMSELPFTIASKRKYL 768

Qy 319 AFWDGSETRKNLECNLCNCNQPPTPVRYRVDMT-----VPTAMWTGGDWLNSNPEDVWMLLSEYT 373

Db 769 GIQLTRDVKDLFKENY-KPLLNEIKEDNWKWNKIPCS-----WVGRINIVKMAI--LP 818

Qy 374 NLTHHKN-IP-----EVAHVDFIWGLDAPH 397

Db 819 KVIVYRFNALPIKLPMTFFTELETTKLF1WNQKRAH 854

Search completed: February 3, 2003, 13:49:16
Job time : 17 secs

GenCore version 5.1.3
 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 3, 2003, 13:47:24 ; Search time 35 Seconds

(without alignments)
 2490.227 Million cell updates/sec

Title: US-09-333-159-47

Scoring table: BLOSUM62
 Perfect score: 2247
 Sequence: 1. MLETLSRQIVSHRMEMVLL.....IHLMQQEETNLSQGRCEAVL 423

Scoring table: BLOSUM62
 Perfect score: 2247
 Sequence: 1. MLETLSRQIVSHRMEMVLL.....IHLMQQEETNLSQGRCEAVL 423

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTRMBL_21:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_invertebrate:*

5: sp_mammal:*

6: sp_mhc:*

7: sp_organelle:*

8: sp_phage:*

9: sp_plant:*

10: sp_rvirus:*

11: sp_virus:*

12: sp_viruse:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriapl:*

17: sp_archeap:*

ALIGNMENTS

RESULTS

1

Q96LG2

ID Q96LG2

AC Q96LG2;

PRELIMINARY;

PRT;

374 AA.

DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DT 01-MAR-2002 (Novel lipase) (Fragment).

GN BA30415_1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID:9606;

RN [1]

RP SEQUENCH FROM N.A.

RA BRAY-ALLEN S.

RL Submitted (AUG-2001) to the EMBL/GenBank/DBBJ databases.

DR EMBL; AL353113; CAC78754_1.

DR InterPro; IPR00073; Abhydrolase.

DR InterPro; IPR00074; Lipase.

DR InterPro; IPR000379; Ser-estrs_site.

DR Pfam; PF00561; abhydrolase_1.

DR PROSITE; PS00120; LIPASE_SEP; UNKNOWN_1.

DR FT NONTER 1 1

DR SEQUNCI; 374 AA; 42371 MW; 5E7220A889437337 CRC64;

DR SQ 88.6%; Score 1991; DB 4; Length 374;

DR Query Match 88.6%; Score 1991; DB 4; Length 374;

DR Best Local Similarity 100.0%; Pred. No. 98-167;

DR Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DR QY 50 SETIQQGQPCPEEYEVATEDGYLSVNRIPRGIVQPKKTGSRPPVLLQHGLYVGASWIS 109

DR 1 SETIQQGQPCPEEYEVATEDGYLSVNRIPRGIVQPKKTGSRPPVLLQHGLYVGASWIS 60

DR DB 110 NLNNNSLGFIILADAGEDWGMGSORGNAWSRKHTLSIDQDEFATFSIDEMARDLPAVN 169

DR DB 61 NLNNNSLGFIILADAGEDWGMGSORGNAWSRKHTLSIDQDEFATFSIDEMARDLPAVN 120

DR QY 170 FIIQKTGQEKKIYVGYSQGTNTGFIASTMPMELAQKIKMYFALAPIATVKHAKSPGTKFL 229

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match Length DB ID Description

1 1991 88.6 374 4 Q96LG2 homo sapien

2 1134.5 50.5 395 11 Q96LG2 homus musculus

3 1134.5 50.5 395 11 Q9d6x0 homus musculus

4 1134.5 50.5 395 11 Q9d6Q6 homus musculus

5 1134.5 50.5 395 11 Q9d6P3 homus musculus

6 1133.5 50.4 395 11 Q9cPP8 homus musculus

7 1133.5 50.4 395 11 Q9cPP7 homus musculus

8 1131.5 50.4 395 11 Q9d6L9 homus musculus

9 1129.5 50.3 395 11 Q9d6T5 homus musculus

10 1128.5 50.2 395 11 Q9d767 homus musculus

11 1127.5 50.2 395 11 Q9d7C5 homus musculus

12 1126.5 50.1 395 11 Q9d766 homus musculus

13 1126.5 50.1 395 11 Q9d6L1 homus musculus

14 1125.5 50.1 395 11 Q9d6Q3 homus musculus

15 1124.5 50.0 395 11 Q9d760 homus musculus

16 1124.5 50.0 395 11 Q9d6S5 homus musculus

RESULT 4		RESULT 5	
09D6Q6	PRELIMINARY;	09D6P3	PRELIMINARY;
09D6Q6;	PRT;	09D6P3	PRT;
01-JUN-2001	(TREMBLrel. 17, Created)	AC	395 AA.
01-MAR-2002	(TREMBLrel. 20, Last annotation update)	Q9D6P3	395 AA.
Adult male tongue cDNA, RIKEN full length enriched library, clone:23100672K20, full insert sequence.		Q9D6P3	395 AA.
2310051B22RIK.		Q9D6P3	395 AA.
Mus musculus (Mouse).		Q9D6P3	395 AA.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		AC	395 AA.
NCBI_TAXID=10096;		Q9D6P3	395 AA.
[1]		Q9D6P3	395 AA.
SEQUENCE FROM N.A.		Q9D6P3	395 AA.
STRAIN=C57BL/6J; TISSUE=TONGUE;		Q9D6P3	395 AA.
MEDLINE=21085660; PubMed=11217851;		Q9D6P3	395 AA.
Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H. A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nakaido I., Pesole G., Quackenbush J., Schriml L. M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blaake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M. F., Brownstein M. J., Bult C., Fletcher C., Fujita M., Garibaldi M., Gustincich S., Hill D., Hoffmann M., Hume D. A., Kamiya M., Lee N. H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Suya T., Shibata Y., Storch K. F., Suzuki H., Toyokuni K., Wang K. H., Weitz C., Whittaker C., Wilmung L., Wunschaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuka S., Hayashizaki Y.;	Q9D6P3	395 AA.	
"Functional annotation of a full-length mouse cDNA collection."		Q9D6P3	395 AA.
Nature 409:685-690(2000).		Q9D6P3	395 AA.
EMBL: AK010093; BAB26597.1; -		Q9D6P3	395 AA.
MGD: MGI:K1914967; 231051B22RIK.		Q9D6P3	395 AA.
InterPro: IPR000073; Abhydrolase.		Q9D6P3	395 AA.
Suzuki H., Tovo-Oka K., Wang K. H., Weitz C., Whittaker C., Williamson K. F.,		Q9D6P3	395 AA.
Gustincich S., Hill D., Hoffmann M., Hume D. A., Kamiya M., Lee N. H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Suya T., Shibata Y., Storch K. F., Suzuki H., Toyokuni K., Wang K. H., Weitz C., Whittaker C., Williamson K. F.,		Q9D6P3	395 AA.

RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,	373 TNLYHKNIPPEAWHVDIFINGLDAPHMYNBIHLMQQE 410
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,	358 PNLLYKEILPYNLDFINAMDAPOEVYNEIVTMWAAED 395
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,	
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,	
RA	Schriml L.M., Staubli R., Tomita M., Wagner L., Wasnio T.,	
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,	
RA	Blake J., Boffelli D., Furuno N., Carninci P., de Bonaldo M.F.,	
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,	
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,	
RA	Lyon S., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,	
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,	
RA	Suzuki H., Sato K., Schoenbach C., Seva T., Shabata Y., Storch K.-F.,	
RA	Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilmung L.,	
RA	Wynshaw-Boris A., Yoshida K., Hassegawa Y., Kawaji H., Kohsueki S.,	
RA	Hayashizaki Y.,	
RT	"Functional annotation of a full-length mouse cDNA collection."	
RL	Nature 408: 65-69 (2001);	
DR	EMBL: AK010236; BAB6787.1;	
DR	EMBL: AK009413; BAB65272.1;	
DR	EMBL: AK009428; BAB6580.1;	
DR	EMBL: AK009459; BAB6300.1;	
DR	EMBL: AK009473; BAB65312.1;	
DR	EMBL: AK009474; BAB65313.1;	
DR	EMBL: AK009479; BAB65316.1;	
DR	EMBL: AK009523; BAB65338.1;	
DR	EMBL: AK009525; BAB65339.1;	
DR	EMBL: AK009546; BAB65352.1;	
DR	EMBL: AK009571; BAB65368.1;	
DR	EMBL: AK009573; BAB65370.1;	
DR	EMBL: AK009579; BAB65466.1;	
DR	EMBL: AK009729; BAB65495.1;	
DR	EMBL: AK009773; BAB65647.1;	
DR	EMBL: AK010119; BAB65647.1;	
DR	EMBL: AK010035; BAB65656.1;	
DR	EMBL: AK010058; BAB65673.1;	
DR	EMBL: AK010661; BAB6575.1;	
DR	EMBL: AK010124; BAB6575.1;	
DR	EMBL: AK010125; BAB65716.1;	
DR	MGI: 1914967; 231051B21R1K.	
DR	InterPro: IPR000073; Abhydrolase.	
DR	InterPro: IPR000734; Lipase.	
DR	InterPro: IPR000379; Ser_estr_s-site.	
DR	PROSITE: PS00120; Lipase_SER; 1.	
SQ	SEQUENCE 395 AA; 44637 MW; D3F9B65EA671E34 CRC64;	
Query	Match 50.4%; Score 1133.5; DB 11; Length 395;	
Best Local Similarity 53.5%; Pred. No. 2.7e-91;		
Matches 213; Conservative 70; Mismatches 108; Indels 7; Gaps 3;		
Db	1 MWLLILVAYMFQ-RVNVSVHMPMTKAVDPFAFMNISEITIQHOGYPCEBEYATEDGYILSY 75	
Db	1 MWLLILVAYMFQ-SVLSAFGGAAGHGFGLGKPKNPEANMNSQMTWYGYSEEVYVTEGYILSY 60	
Qy	76 NRIPGCLVQPKKTTGSRPVLLQHGLYGVASNWISLPLNSLGFILADGEFDWGNNSRGN 135	
Qy	61 YRIPGKVNSENIGRPAVALQHGLIASATNWNLPLNSLAFILADGVDWGNNSRGN 120	
Qy	136 AWSRKHTLSDQDFWAFSYDEMARDLPAVINFILQTKTQEKIYVGSOGTTMGFIA 195	
Db	121 TWSRKNVYYSPDSVETWAFSEDEMAYDLPATIDFIVKQGKEITHYHSQGTIGFIA 180	
Qy	196 FSTMPPELAQKTKMYPALAPATVHKAKSPGTKEFLPDMIKLGKKEFL--YQTREL 252	
Db	181 FSTNPALAKKTKRFLAPATVKTSPFKKISLIPKFELKVFGNKNMFPNHYLDQFL 240	
Qy	253 RQLYLQGVOVLDQICSNMILJUGFNTNNMRSRAHTLAGTSVONLJHWSQAV 312	
Db	241 GTEV---CSRELDLICSNALFIFCGEDKKLNLYSREDVYLGHPAGTSDQFLHWQLA 297	
Qy	313 NSGEIRAFDGSSETKLNKRCNQPTPVYRVRDMTPAATWGGQDWLSNPEDVYKMLSEV 372	
Db	298 KSGKQAYANGSPLONMHLYNQKTPPYDVSAMTVPIAVWNGHDILADQDMLPKL 357	
Qy	358 PNLLYKEILPYNLDFINAMDAPOEVYNEIVTMWAAED 395	
Db	Q9D6L9 PRELIMINARY; PRT; 395 AA.	
Db	Q9D6L9 ID PRELIMINARY; PRT; 395 AA.	
AC	09D6L9 AC 09D6L9	
DT	01-JUN-2001 (TREMBLrel. 17, Created)	
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)	
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)	
DE	Adult male tongue cDNA, RIKEN full-length enriched library clone: 2310076L13, full-insert sequence.	
DE	clone: 2310051B21R1K.	
GN	Mus musculus (Mouse).	
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OC	NCBI_TaxID=10090;	
OC	NCBI_TaxID=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=C57BL/6J; TISSUE=TONGUE;	
RX	MEDLINE=2108560; PubMed=11217851;	
RA	Kawai J., Shiozawa A., Shibata K., Yoshino M., Itoh M., Ishii M., Fukunishi Y., Konno H., Adachi J., Kondo S., Yamanaka I., Arakawa T., Hara A., Fukunawa T., Bono H., Kasukawa T., Saito R., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tonita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Rodriguez L., Saksela H., Sato K., Schoenbach C., Seya T., Shabata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.;	
RA	"Functional annotation of a full-length mouse cDNA collection."	
RA	Nature 408: 65-69 (2001);	
RA	EMBL: AK010236; BAB6787.1;	
RA	EMBL: AK009413; BAB65272.1;	
RA	EMBL: AK009428; BAB6580.1;	
RA	EMBL: AK009459; BAB6300.1;	
RA	EMBL: AK009473; BAB65312.1;	
RA	EMBL: AK009474; BAB65313.1;	
RA	EMBL: AK009479; BAB65316.1;	
RA	EMBL: AK009523; BAB65338.1;	
RA	EMBL: AK009525; BAB65339.1;	
RA	EMBL: AK009546; BAB65352.1;	
RA	EMBL: AK009571; BAB65368.1;	
RA	EMBL: AK009573; BAB65370.1;	
RA	EMBL: AK009729; BAB6466.1;	
RA	EMBL: AK009773; BAB65495.1;	
RA	EMBL: AK010119; BAB65647.1;	
RA	EMBL: AK010035; BAB65656.1;	
RA	EMBL: AK010058; BAB65673.1;	
RA	EMBL: AK010661; BAB6575.1;	
RA	EMBL: AK010124; BAB6575.1;	
RA	EMBL: AK010125; BAB65716.1;	
RA	MGI: 1914967; 231051B21R1K.	
DR	InterPro: IPR000073; Abhydrolase.	
DR	InterPro: IPR000734; Lipase.	
DR	InterPro: IPR000379; Ser_estr_s-site.	
DR	PROSITE: PS00120; Lipase_SER; 1.	
DR	DR "Functional annotation of a full-length mouse cDNA collection."	
DR	DR EMBL: AK010203; BAB6766.1;	
DR	DR MGDB: MGI:1914967; 231051B21R1K.	
DR	DR InterPro: IPR000073; Abhydrolase.	
DR	DR InterPro: IPR000734; Lipase.	
DR	DR InterPro: IPR000379; Ser_estr_s-site.	
DR	DR Pfam: PF00561; abhydrolase; 1.	
DR	DR PROSITE: PS00120; Lipase_SER; 1.	
DR	DR RBL: Nature 409:685-690 (2001).	
DR	DR MGI: MGI:1914967; 231051B21R1K.	
DR	DR InterPro: IPR000073; Abhydrolase.	
DR	DR InterPro: IPR000734; Lipase.	
DR	DR InterPro: IPR000379; Ser_estr_s-site.	
DR	DR Pfam: PF00561; abhydrolase; 1.	
DR	DR PROSITE: PS00120; Lipase_SER; 1.	
DR	DR RBL: Nature 409:685-690 (2001).	
DR	DR MGI: MGI:1914967; 231051B21R1K.	
DR	DR InterPro: IPR000073; Abhydrolase.	
DR	DR InterPro: IPR000734; Lipase.	
DR	DR InterPro: IPR000379; Ser_estr_s-site.	
DR	DR Pfam: PF00561; abhydrolase; 1.	
DR	DR PROSITE: PS00120; Lipase_SER; 1.	
DR	DR RBL: Nature 409:685-690 (2001).	
DR	DR MGI: MGI:1914967; 231051B21R1K.	
DR	DR InterPro: IPR000073; Abhydrolase.	
DR	DR InterPro: IPR000734; Lipase.	
DR	DR InterPro: IPR000379; Ser_estr_s-site.	
DR	DR Pfam: PF00561; abhydrolase; 1.	
DR	DR PROSITE: PS00120; Lipase_SER; 1.	
DR	DR RBL: Nature 409:685-690 (2001).	
DR	DR MGI: MGI:1914967; 231051B21R1K.	
DR	DR InterPro: IPR000073; Abhydrolase.	
DR	DR InterPro: IPR000734; Lipase.	
DR	DR InterPro: IPR000379; Ser_estr_s-site.	
DR	DR Pfam: PF00561; abhydrolase; 1.	
DR	DR PROSITE: PS00120; Lipase_SER; 1.	
DR	DR RBL: Nature 409:685-690 (2001).	
DR	DR MGI: MGI:1914967; 231051B21R1K.	
DR	DR InterPro: IPR000073; Abhydrolase.	
DR	DR InterPro: IPR000734; Lipase.	
DR	DR InterPro: IPR000379; Ser_estr_s-site.	
DR	DR Pfam: PF00561; abhydrolase; 1.	
DR	DR PROSITE: PS00120; Lipase_SER; 1.	
DR	DR RBL: Nature 409:685-690 (2001).	
DR	DR MGI: MGI:1914967; 231051B21R1K.	
DR	DR InterPro: IPR000073; Abhydrolase.	
DR	DR InterPro: IPR000734; Lipase.	
DR	DR InterPro: IPR000379; Ser_estr_s-site.	
DR	DR Pfam: PF00561; abhydrolase; 1.	
DR	DR PROSITE: PS00120; Lipase_SER; 1.	
DR	DR RBL: Nature 409:685-690 (2001).	
DR	DR MGI: MGI:1914967; 231051B21R1K.	
DR	DR InterPro: IPR000073; Abhydrolase.	
DR	DR InterPro: IPR000734; Lipase.	
DR	DR InterPro: IPR000379; Ser_estr_s-site.	
DR	DR Pfam: PF00561; abhydrolase; 1.	
DR	DR PROSITE: PS00120; Lipase_SER; 1.	
DR	DR RBL: Nature 409:685-690 (2001).	
DR	DR MGI: MGI:1914967; 231051B21R1K.	
DR	DR InterPro: IPR000073; Abhydrolase.	
DR	DR InterPro: IPR000734; Lipase.	
DR	DR InterPro: IPR000379; Ser_estr_s-site.	
DR	DR Pfam: PF00561; abhydrolase; 1.	
DR	DR PROSITE: PS00120; Lipase_SER; 1.	
DR	DR RBL: Nature 409:685-690 (2001).	
DR	DR MGI: MGI:1914967; 231051B21R1K.	
DR	DR InterPro: IPR000073; Abhydrolase.	
DR	DR InterPro: IPR000734; Lipase.	
DR	DR InterPro: IPR000379; Ser_estr_s-site.	
DR	DR Pfam: PF00561; abhydrolase; 1.	
DR	DR PROSITE: PS00120; Lipase_SER; 1.	
DR	DR RBL: Nature 409:685-690 (2001).	
DR	DR MGI: MGI:1914967; 231051B21R1K.	
DR	DR InterPro: IPR000073; Abhydrolase.	
DR	DR InterPro: IPR000734; Lipase.	
DR	DR InterPro: IPR000379; Ser_estr_s-site.	
DR	DR Pfam: PF00561; abhydrolase; 1.	
DR	DR PROSITE: PS00120; Lipase_SER; 1.	
DR	DR RBL: Nature 409:685-690 (2001).	
DR	DR MGI: MGI:1914967; 231051B21R1K.	
DR	DR InterPro: IPR000073; Abhydrolase.	
DR	DR InterPro: IPR000734; Lipase.	
DR	DR InterPro: IPR000379; Ser_estr_s-site.	
DR	DR Pfam: PF00561; abhydrolase; 1.	
DR	DR PROSITE: PS00120; Lipase_SER; 1.	
DR	DR RBL: Nature 409:685-690 (2001).	
DR	DR MGI: MGI:1914967; 231051B21R1K.	
DR	DR InterPro: IPR000073; Abhydrolase.	
DR	DR InterPro: IPR000734; Lipase.	
DR	DR InterPro: IPR000379; Ser_estr_s-site.	
DR	DR Pfam: PF00561; abhydrolase; 1.	
DR	DR PROSITE: PS00120; Lipase_SER; 1.	
DR	DR RBL: Nature 409:685-690 (2001).	
DR	DR MGI: MGI:1914967; 231051B21R1K.	
DR	DR InterPro: IPR000073; Abhydrolase.	
DR	DR InterPro: IPR000734; Lipase.	
DR	DR InterPro: IPR000379; Ser_estr_s-site.	
DR	DR Pfam: PF00561; abhydrolase; 1.	
DR	DR PROSITE: PS00120; Lipase_SER; 1.	
DR	DR RBL: Nature 409:685-690 (2001).	
DR	DR MGI: MGI:1914967; 231051B21R1K.	
DR	DR InterPro: IPR000073; Abhydrolase.	
DR	DR InterPro: IPR000734; Lipase.	
DR	DR InterPro: IPR000379; Ser_estr_s-site.	
DR	DR Pfam: PF00561; abhydrolase; 1.	
DR	DR PROSITE: PS00120; Lipase_SER; 1.	
DR	DR RBL: Nature 409:685-690 (2001).	
DR	DR MGI: MGI:1914967; 231051B21R1K.	
DR	DR InterPro: IPR000073; Abhydrolase.	
DR	DR InterPro: IPR000734; Lipase.	
DR	DR InterPro: IPR000379; Ser_estr_s-site.	
DR	DR Pfam: PF00561; abhydrolase; 1.	
DR	DR PROSITE: PS00120; Lipase_SER; 1.	
DR	DR RBL: Nature 409:685-690 (2001).	
DR	DR MGI: MGI:1914967; 231051B21R1K.	
DR	DR InterPro: IPR000073; Abhydrolase.	
DR	DR InterPro: IPR000734; Lipase.	
DR	DR InterPro: IPR000379; Ser_estr_s-site.	
DR	DR Pfam: PF00561; abhydrolase; 1.	
DR	DR PROSITE: PS00120; Lipase_SER; 1.	
DR	DR RBL: Nature 409:685-690 (2001).	
DR	DR MGI: MGI:1914967; 231051B21R1K.	
DR	DR InterPro: IPR000073; Abhydrolase.	
DR	DR InterPro: IPR000734; Lipase.	
DR	DR InterPro: IPR000379; Ser_estr_s-site.	
DR	DR Pfam: PF00561; abhydrolase; 1.	
DR	DR PROSITE: PS00120; Lipase_SER; 1.	
DR	DR RBL: Nature 409:685-690 (2001).	
DR	DR MGI: MGI:1914967; 231051B21R1K.	
DR	DR InterPro: IPR000073; Abhydrolase.	
DR	DR InterPro: IPR000734; Lipase.	
DR	DR InterPro: IPR000379; Ser_estr_s-site.	
DR	DR Pfam: PF00561; abhydrolase; 1.	
DR	DR PROSITE: PS00120; Lipase_SER; 1.	
DR	DR RBL: Nature 409:685-690 (2001).	
DR	DR MGI: MGI:1914967; 231051B21R1K.	
DR	DR InterPro: IPR000073; Abhydrolase.	
DR	DR InterPro: IPR000734; Lipase.	
DR	DR InterPro: IPR000379; Ser_estr_s-site.	
DR	DR Pfam: PF00561; abhydrolase; 1.	
DR	DR PROSITE: PS00120; Lipase_SER; 1.	
DR	DR RBL: Nature 409:685-690 (2001).	
DR	DR MGI: MGI:1914967; 231051B21R1K.	
DR	DR InterPro: IPR000073; Abhydrolase.	
DR	DR InterPro: IPR000734; Lipase.	
DR	DR InterPro: IPR000379; Ser_estr_s-site.	
DR	DR Pfam: PF00561; abhydrolase; 1.	
DR	DR PROSITE: PS00120; Lipase_SER; 1.	
DR	DR RBL: Nature 409:685-690 (2001).	
DR	DR MGI: MGI:1914967; 231051B21R1K.	
DR	DR InterPro: IPR000073; Abhydrolase.	
DR	DR InterPro: IPR000734; Lipase.	
DR	DR InterPro: IPR000379; Ser_estr_s-site.	
DR	DR Pfam: PF00561; abhydrolase; 1.	
DR	DR PROSITE: PS00120; Lipase_SER; 1.	
DR	DR RBL: Nature 409:685-690 (2001).	
DR	DR MGI: MGI:1914967; 231051B21R1K.	
DR	DR InterPro: IPR000073; Abhydrolase.	
DR	DR InterPro: IPR000734; Lipase.	
DR	DR InterPro: IPR000379; Ser_estr_s-site.	
DR	DR Pfam: PF00561; abhydrolase; 1.	
DR	DR PROSITE: PS00120; Lipase_SER; 1.	
DR</td		

Db	241	GTEV--CSREILDLCSNAFICGFDKKLNKCNQPTPYRVDMTYPTAMTGGQDNLSNPDVKMLSEV	372	Db	121	TWSRKVVYSSPDSVEFWAFSDEMAKYDLPATIDFYQKTCQEQKTHYVGHQSQGTIGFIA	180	
Qy	313	NSGEILRAFDNGSETKNIKEKCNQPTPYRVDMTYPTAMTGGQDNLSNPDVKMLSEV	372	Qy	196	FSTMPDEAQKIRMYFALAPITVYKAKSPGKFLLPDMMMKGLFKEFL--YQTRFL	252	
Db	298	KSGKLOAYNWSPLQNLHYQKTPPYDVSAMTPTAVWNGHDLADPODVAMLLPKL	357	Db	181	FSTNPALAKIKRKYFALAPATVYKTESPFKISLSPKFLLKVFQNKMPHNYLDQFL	240	
Qy	373	TNLVYHKNIPEWAHYDFTWGLDAPHMYNEIHLMMQEE	410	Qy	253	ROLIVYLGQYILDQICNSINMILLGGFTNTNNNNMSRASVYPAHTLAGTSVYONLHWSQAV	312	
Db	358	PNLLYKIREILYHNLDITWANDAPQEVYNEIYTMMAED	395	Db	241	GREV--CSREILDLCSNAFICFGDFDKNNLNVSFDPVYLGHNPAAGTSDCFLFHQAQLA	297	
RESULT 9								
Q9D6T5	Q9D6T5;	PRELIMINARY;	PRT;	395 AA.	Qy	313	NGELRAFDNGSETKNEKQPTPYRVDMTYPTAMTGGQDKLNSNPDVKMLSEV	372
AC	Q9D6T5;				Qy	358	PNLLYKIREILYHNLDITWANDAPQEVYNEIYTMMAED	395
DT	01-JUN-2001	(TREMBLrel. 17, Created)	DT	358	PNTLYKIREILYHNLDITWANDAPQEVYNEIYTMMAED	395		
DT	01-JUN-2001	(TREMBLrel. 17, Last sequence update)	DT	395 AA.				
DT	01-MAR-2002	(TREMBLrel. 20, Last annotation update)	DT					
DE	Adult male tongue cDNA, REKEN full-length enriched library,		DE					
DE	clone:2310061A13, full insert sequence.		DE					
GN	2310061A13;		GN					
OS	Mus musculus (Mouse)		OS					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		OC					
OC	Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.		OC					
QX	NCBI_TaxID=10090;		QX					
RN	[1]		RN					
RP	SEQUENCE FROM N.A.		RP					
RC	STRAIN=C57BL/6J; TISSUE="TONGUE";		RC					
RX	MEDLINE:21085660; Published=11217851;		RX					
RA	Kawai J., Shinagawa A., Shibusawa K., Yoshino M., Itoh M., Ishii Y.,		RA					
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,		RA					
RA	Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto I.,		RA					
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,		RA					
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,		RA					
RA	Pleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,		RA					
RA	Kueh P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,		RA					
RA	Schrimali L.M., Straubli F., Suzuki R., Tomita M., Wagner L., Washio T.,		RA					
RA	Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,		RA					
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,		RA					
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,		RA					
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,		RA					
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombretti P.,		RA					
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,		RA					
RA	Sasaki H., Sato K., Schoenbach C., Seyta T., Shiba Y., Storch K.-P.,		RA					
RA	Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Wilming L.,		RA					
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,		RA					
RA	Hayashizaki Y.,		RA					
RT	Functional annotation of a full-length mouse cDNA collection.";		RT					
RL	Nature 349:885-890(2001).		RL					
DR	EMBL: AK009990; BAB26629.1; -		DR					
DR	InterPro: IPR00073; Abhydrolase.		DR					
DR	InterPro: IPR00074; Lipase.		DR					
DR	InterPro: IPR00039; Ser.estrs_site.		DR					
DR	Pfam: PF00561; abhydrolase_1.		DR					
DR	PROSITE: PS00120; LIPASE_SER; 1.		DR					
SEQUENCE	395 AA;	D3F96DB83161C3EF CRC64;	SEQUENCE	395 AA;	44623 MW;	E43317C2254FA8FB CRC64;	SEQUENCE	
SQ			SQ					
Query Match	50.3%	Score 1129.5; DB 11; Length 395;	Query Match	50.2%	Score 1128.5; DB 11; Length 395;			
Best Local Similarity	53.3%	Pred. No. 6.e-91;	Best Local Similarity	53.3%	Pred. No. 7.e-91;			
Matches 212;	Conservative	Indels 7; Gaps 3;	Matches 212;	Conservative	70; Mismatches 109; Indels 7; Gaps 3;			
Qy	17 MNLILVAYMFQ RAVNSVHMPKAVDPEAFMNISEIIQHQGPCEEVEATEDGYILSV	75	Qy	17 MWLILVAYMFQ RAVNSVHMPKAVDPEAFMNISEIIQHQGPCEEVEATEDGYILSV	75			
Db	1 MNLLVTSVLSAFAFGAAGLGLFGKLGPKNPEANNNVQMTWYGPSEEVEYVTDGYILGV	60	Db	1 MNLLVTSVLSAFAFGAAGLGLFGKLGPKNPEANNNVQMTWYGPSEEVEYVTDGYILGV	60			
Qy	76 NRPLRGLVQPKITGSPRVVLLQHLYGSGASNNLNPNSLGFYDWMGNRGN	135	Qy	136 ANSRKHTLSDODEWAFSYDEMAREDLPAVINFILQTKGQEKKIYVGYSQGTNGFIA	195			
Db	61 YRIPYKGNSENIGKRPAYLQHLLISATNWPNLPSAFLADGTDWLNRSRGN	120	Db	1 MWLILVAYMFQ RAVNSVHMPKAVDPEAFMNISEIIQHQGPCEEVEATEDGYILGV	60			

DR	Pfam:PF00561; abhydrolase; 1.	RT	"Functional annotation of a full-length mouse cDNA collection.";
DR	PROSITE; PS00120; LIPISE_SER; 1.	RL	Nature 409:685-690(2001).
SO	SEQUENCE 395 AA; 44648 MW; CC6987553AA7A4 CRC64;	DR	EMBL; AK010231; BA226784.1;
Query Match	50.1%; Score 1126.5; DB 11; Length 395;	DR	MGI; MGI-191467; 2310051B21R1K.
Best Local Similarity	53.3%; Pred. No. 1.1e-90;	DR	InterPro; IPR00073; Abhydrolase.
Matches	212; Conservative 70; Mismatches 109; Indels 7; Gaps 3;	DR	InterPro; IPR000734; Lipase.
Qy	17 MWLILVAYMFO-RNVSYHMPKAVDPFAFMNSEEIIQHGYCPEEVATEDGYILSV 75	DR	InterPro; IPR000379; Ser_estrs_site.
Db	1 MWLILVTSVLSAFGGAHGLEGKLGPKPNPANMNSQMTYWGIFSEEEVTTEDGYILGV 60	DR	Pfam; PF00561; abhydrolase; 1.
Qy	76 NRIPGLYQPKKTGSRPVYLLQHGGASNWNISNLPNNSLGFITADAGFDVYNGNSRGN 135	DR	PROSITE; PS00120; LIPISE_SER; 1.
Db	61 YRIPGKKNSEIGNGRPVAYLLHGIIASATWNLPNNSLAFIADGYDWLGNNSRGN 120	DR	SEQUENCE 395 AA; 44659 MW; 13E0B95FC5A0E0 CRC64;
Qy	136 AWSRKHKTLSIDQDEFWASYDENBARFDPAVINFLQTKGOEKKYYGKSGQTGMGFA 195	Query Match	50.1%; Score 1126.5; DB 11; Length 395;
Db	121 TWSRANVYSPDSVSEWAFSDEKAYDLPATIDFIVQTKGOEKKHYGHSGQTGIFTA 180	Best Local Similarity	53.5%; Pred. No. 1.1e-90;
Qy	196 FSTMPBLAQKIKMFALATVKAHKSPOTKFLLPDMIKGLGKKEFL---YQTRFL 252	Matches	213; Conservative 60; Mismatches 109; Indels 7; Gaps 3;
Db	181 FSTMPALAKKIKREYALAPVATVYTESFFKKISLIPKFLKVEFGNKIFMPYNYLDQFL 240	Qy	17 MWLILVAYMFO-RNVSYHMPKAVDPFAFMNSEEIIQHGYCPEEVATEDGYILSV 75
Qy	253 RQLVYLCGQVILDQICSNIMLLQGENTNNMNSRASYVAHTLAGTSVQNLHWSQAV 312	Db	1 MWLILVTSVLSAFGGAHGLEGKLGPKPNPANMNSQMTYWGIFSEEEVTTEDGYILGV 60
Db	241 GTEV--CSRELLDLCNSLAFIPOGFDDKNNYNSRFDVLYHNPAGTSTQDLPWAQLA 297	Qy	76 NRIPGLYQEKKTGSRPVYLLQHGGASNWNISNLPNNSLGFITADAGFDVYNGNSRGN 135
Qy	313 NGTETRAFDGSEKMLNLECNQNPVPRVYRDMYPTAATWGGQWLSNPEDVYMLLSEV 372	Db	61 YRIPGKKNSEIGNGRPVAYLLHGIIASATWNLPNNSLAFIADGYDWLGNNSRGN 120
Db	298 KSGKQAYNNGSPSPLQHMLNHYQKTPPYDVSAMTPVIAVNGGHDILADQDVAMLLPKL 357	Qy	196 FSTMPBLAQKIKMFALATVKAHKSPOTKFLLPDMIKGLGKKEFL---YQTRFL 252
Qy	373 TNLIYHKNIPERAWHNDINGLDAPHRYMNEYIHLHQQE 410	Db	61 YRIPGKKNSEIGNGRPVAYLLHGIIASATWNLPNNSLAFIADGYDWLGNNSRGN 120
Db	358 PNLLYHKELLPYHNLDFINWMDAPQEVYNEIVTMMAED 395	Qy	136 AWSRKHKTLSIDQDEFWASYDENBARFDPAVINFLQTKGOEKKYYGKSGQTGMGFA 195
RESULT 13		Db	121 TWSRANVYSPDSVSEWAFSDEKAYDLPATIDFIVQTKGOEKKHYGHSGQTGIFTA 180
Q9D6L1	PRELIMINARY; PRT; 395 AA.	Qy	196 FSTMPBLAQKIKMFALATVKAHKSPOTKFLLPDMIKGLGKKEFL---YQTRFL 252
AC	Q9D6L1;	Db	61 YRIPGKKNSEIGNGRPVAYLLHGIIASATWNLPNNSLAFIADGYDWLGNNSRGN 120
DT	01-JUN-2001 (TREMBLrel. 17, Created)	Qy	136 AWSRKHKTLSIDQDEFWASYDENBARFDPAVINFLQTKGOEKKYYGKSGQTGMGFA 195
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)	Db	121 TWSRANVYSPDSVSEWAFSDEKAYDLPATIDFIVQTKGOEKKHYGHSGQTGIFTA 180
DE	01-MAR-2002 (TREMBLrel. 20, Last annotation update)	Qy	196 FSTMPBLAQKIKMFALATVKAHKSPOTKFLLPDMIKGLGKKEFL---YQTRFL 252
DE	Adult male tongue cDNA, RIKEN full-length enriched library, clone:231007902, full insert sequence.	Db	61 YRIPGKKNSEIGNGRPVAYLLHGIIASATWNLPNNSLAFIADGYDWLGNNSRGN 120
DE	2310051B21R1K.	Qy	136 AWSRKHKTLSIDQDEFWASYDENBARFDPAVINFLQTKGOEKKYYGKSGQTGMGFA 195
OS	Mus musculus (Mouse).	Db	121 TWSRANVYSPDSVSEWAFSDEKAYDLPATIDFIVQTKGOEKKHYGHSGQTGIFTA 180
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Qy	196 FSTMPBLAQKIKMFALATVKAHKSPOTKFLLPDMIKGLGKKEFL---YQTRFL 252
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	Db	61 YRIPGKKNSEIGNGRPVAYLLHGIIASATWNLPNNSLAFIADGYDWLGNNSRGN 120
OX	Aizawa K., Izawa M., Nishi K., Kiyoosawa H., Kondo S., Yamanka I.,	Qy	136 AWSRKHKTLSIDQDEFWASYDENBARFDPAVINFLQTKGOEKKYYGKSGQTGMGFA 195
RN	Saito T., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,	Db	121 TWSRANVYSPDSVSEWAFSDEKAYDLPATIDFIVQTKGOEKKHYGHSGQTGIFTA 180
RP	RAKuroda Y., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,	Qy	196 FSTMPBLAQKIKMFALATVKAHKSPOTKFLLPDMIKGLGKKEFL---YQTRFL 252
RC	RAKuroda Y., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,	Db	61 YRIPGKKNSEIGNGRPVAYLLHGIIASATWNLPNNSLAFIADGYDWLGNNSRGN 120
RX	RAXawa J., Shinagawa A., Shibusawa K., Itoh M., Ishii Y.,	Qy	136 AWSRKHKTLSIDQDEFWASYDENBARFDPAVINFLQTKGOEKKYYGKSGQTGMGFA 195
RA	RAXawa T., Hara A., Fukunishi Y., Konno H., Kondo H., Adachi J., Fukuda S.,	Db	121 TWSRANVYSPDSVSEWAFSDEKAYDLPATIDFIVQTKGOEKKHYGHSGQTGIFTA 180
RA	RAXarai K., Okido T., Furuno M., Aono H., Batalov R., Barsh G.,	Qy	196 FSTMPBLAQKIKMFALATVKAHKSPOTKFLLPDMIKGLGKKEFL---YQTRFL 252
RA	RAXarai K., Matsuda H.A., Gojobori T., Bono H., Kasukawa T., Saito R.,	Db	61 YRIPGKKNSEIGNGRPVAYLLHGIIASATWNLPNNSLAFIADGYDWLGNNSRGN 120
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Qy	136 AWSRKHKTLSIDQDEFWASYDENBARFDPAVINFLQTKGOEKKYYGKSGQTGMGFA 195
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Db	121 TWSRANVYSPDSVSEWAFSDEKAYDLPATIDFIVQTKGOEKKHYGHSGQTGIFTA 180
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Qy	196 FSTMPBLAQKIKMFALATVKAHKSPOTKFLLPDMIKGLGKKEFL---YQTRFL 252
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Db	61 YRIPGKKNSEIGNGRPVAYLLHGIIASATWNLPNNSLAFIADGYDWLGNNSRGN 120
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Qy	136 AWSRKHKTLSIDQDEFWASYDENBARFDPAVINFLQTKGOEKKYYGKSGQTGMGFA 195
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Db	121 TWSRANVYSPDSVSEWAFSDEKAYDLPATIDFIVQTKGOEKKHYGHSGQTGIFTA 180
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Qy	196 FSTMPBLAQKIKMFALATVKAHKSPOTKFLLPDMIKGLGKKEFL---YQTRFL 252
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Db	61 YRIPGKKNSEIGNGRPVAYLLHGIIASATWNLPNNSLAFIADGYDWLGNNSRGN 120
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Qy	136 AWSRKHKTLSIDQDEFWASYDENBARFDPAVINFLQTKGOEKKYYGKSGQTGMGFA 195
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Db	121 TWSRANVYSPDSVSEWAFSDEKAYDLPATIDFIVQTKGOEKKHYGHSGQTGIFTA 180
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Qy	196 FSTMPBLAQKIKMFALATVKAHKSPOTKFLLPDMIKGLGKKEFL---YQTRFL 252
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Db	61 YRIPGKKNSEIGNGRPVAYLLHGIIASATWNLPNNSLAFIADGYDWLGNNSRGN 120
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Qy	136 AWSRKHKTLSIDQDEFWASYDENBARFDPAVINFLQTKGOEKKYYGKSGQTGMGFA 195
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Db	121 TWSRANVYSPDSVSEWAFSDEKAYDLPATIDFIVQTKGOEKKHYGHSGQTGIFTA 180
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Qy	196 FSTMPBLAQKIKMFALATVKAHKSPOTKFLLPDMIKGLGKKEFL---YQTRFL 252
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Db	61 YRIPGKKNSEIGNGRPVAYLLHGIIASATWNLPNNSLAFIADGYDWLGNNSRGN 120
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Qy	136 AWSRKHKTLSIDQDEFWASYDENBARFDPAVINFLQTKGOEKKYYGKSGQTGMGFA 195
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Db	121 TWSRANVYSPDSVSEWAFSDEKAYDLPATIDFIVQTKGOEKKHYGHSGQTGIFTA 180
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Qy	196 FSTMPBLAQKIKMFALATVKAHKSPOTKFLLPDMIKGLGKKEFL---YQTRFL 252
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Db	61 YRIPGKKNSEIGNGRPVAYLLHGIIASATWNLPNNSLAFIADGYDWLGNNSRGN 120
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Qy	136 AWSRKHKTLSIDQDEFWASYDENBARFDPAVINFLQTKGOEKKYYGKSGQTGMGFA 195
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Db	121 TWSRANVYSPDSVSEWAFSDEKAYDLPATIDFIVQTKGOEKKHYGHSGQTGIFTA 180
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Qy	196 FSTMPBLAQKIKMFALATVKAHKSPOTKFLLPDMIKGLGKKEFL---YQTRFL 252
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Db	61 YRIPGKKNSEIGNGRPVAYLLHGIIASATWNLPNNSLAFIADGYDWLGNNSRGN 120
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Qy	136 AWSRKHKTLSIDQDEFWASYDENBARFDPAVINFLQTKGOEKKYYGKSGQTGMGFA 195
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Db	121 TWSRANVYSPDSVSEWAFSDEKAYDLPATIDFIVQTKGOEKKHYGHSGQTGIFTA 180
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Qy	196 FSTMPBLAQKIKMFALATVKAHKSPOTKFLLPDMIKGLGKKEFL---YQTRFL 252
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Db	61 YRIPGKKNSEIGNGRPVAYLLHGIIASATWNLPNNSLAFIADGYDWLGNNSRGN 120
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Qy	136 AWSRKHKTLSIDQDEFWASYDENBARFDPAVINFLQTKGOEKKYYGKSGQTGMGFA 195
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Db	121 TWSRANVYSPDSVSEWAFSDEKAYDLPATIDFIVQTKGOEKKHYGHSGQTGIFTA 180
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Qy	196 FSTMPBLAQKIKMFALATVKAHKSPOTKFLLPDMIKGLGKKEFL---YQTRFL 252
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Db	61 YRIPGKKNSEIGNGRPVAYLLHGIIASATWNLPNNSLAFIADGYDWLGNNSRGN 120
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Qy	136 AWSRKHKTLSIDQDEFWASYDENBARFDPAVINFLQTKGOEKKYYGKSGQTGMGFA 195
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Db	121 TWSRANVYSPDSVSEWAFSDEKAYDLPATIDFIVQTKGOEKKHYGHSGQTGIFTA 180
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Qy	196 FSTMPBLAQKIKMFALATVKAHKSPOTKFLLPDMIKGLGKKEFL---YQTRFL 252
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Db	61 YRIPGKKNSEIGNGRPVAYLLHGIIASATWNLPNNSLAFIADGYDWLGNNSRGN 120
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Qy	136 AWSRKHKTLSIDQDEFWASYDENBARFDPAVINFLQTKGOEKKYYGKSGQTGMGFA 195
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Db	121 TWSRANVYSPDSVSEWAFSDEKAYDLPATIDFIVQTKGOEKKHYGHSGQTGIFTA 180
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Qy	196 FSTMPBLAQKIKMFALATVKAHKSPOTKFLLPDMIKGLGKKEFL---YQTRFL 252
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Db	61 YRIPGKKNSEIGNGRPVAYLLHGIIASATWNLPNNSLAFIADGYDWLGNNSRGN 120
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Qy	136 AWSRKHKTLSIDQDEFWASYDENBARFDPAVINFLQTKGOEKKYYGKSGQTGMGFA 195
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Db	121 TWSRANVYSPDSVSEWAFSDEKAYDLPATIDFIVQTKGOEKKHYGHSGQTGIFTA 180
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Qy	196 FSTMPBLAQKIKMFALATVKAHKSPOTKFLLPDMIKGLGKKEFL---YQTRFL 252
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Db	61 YRIPGKKNSEIGNGRPVAYLLHGIIASATWNLPNNSLAFIADGYDWLGNNSRGN 120
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Qy	136 AWSRKHKTLSIDQDEFWASYDENBARFDPAVINFLQTKGOEKKYYGKSGQTGMGFA 195
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Db	121 TWSRANVYSPDSVSEWAFSDEKAYDLPATIDFIVQTKGOEKKHYGHSGQTGIFTA 180
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Qy	196 FSTMPBLAQKIKMFALATVKAHKSPOTKFLLPDMIKGLGKKEFL---YQTRFL 252
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Db	61 YRIPGKKNSEIGNGRPVAYLLHGIIASATWNLPNNSLAFIADGYDWLGNNSRGN 120
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Qy	136 AWSRKHKTLSIDQDEFWASYDENBARFDPAVINFLQTKGOEKKYYGKSGQTGMGFA 195
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Db	121 TWSRANVYSPDSVSEWAFSDEKAYDLPATIDFIVQTKGOEKKHYGHSGQTGIFTA 180
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Qy	196 FSTMPBLAQKIKMFALATVKAHKSPOTKFLLPDMIKGLGKKEFL---YQTRFL 252
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Db	61 YRIPGKKNSEIGNGRPVAYLLHGIIASATWNLPNNSLAFIADGYDWLGNNSRGN 120
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Qy	136 AWSRKHKTLSIDQDEFWASYDENBARFDPAVINFLQTKGOEKKYYGKSGQTGMGFA 195
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Db	121 TWSRANVYSPDSVSEWAFSDEKAYDLPATIDFIVQTKGOEKKHYGHSGQTGIFTA 180
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Qy	196 FSTMPBLAQKIKMFALATVKAHKSPOTKFLLPDMIKGLGKKEFL---YQTRFL 252
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Db	61 YRIPGKKNSEIGNGRPVAYLLHGIIASATWNLPNNSLAFIADGYDWLGNNSRGN 120
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Qy	136 AWSRKHKTLSIDQDEFWASYDENBARFDPAVINFLQTKGOEKKYYGKSGQTGMGFA 195
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Db	121 TWSRANVYSPDSVSEWAFSDEKAYDLPATIDFIVQTKGOEKKHYGHSGQTGIFTA 180
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Qy	196 FSTMPBLAQKIKMFALATVKAHKSPOTKFLLPDMIKGLGKKEFL---YQTRFL 252
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Db	61 YRIPGKKNSEIGNGRPVAYLLHGIIASATWNLPNNSLAFIADGYDWLGNNSRGN 120
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Qy	136 AWSRKHKTLSIDQDEFWASYDENBARFDPAVINFLQTKGOEKKYYGKSGQTGMGFA 195
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Db	121 TWSRANVYSPDSVSEWAFSDEKAYDLPATIDFIVQTKGOEKKHYGHSGQTGIFTA 180
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Qy	196 FSTMPBLAQKIKMFALATVKAHKSPOTKFLLPDMIKGLGKKEFL---YQTRFL 252
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Db	61 YRIPGKKNSEIGNGRPVAYLLHGIIASATWNLPNNSLAFIADGYDWLGNNSRGN 120
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Qy	136 AWSRKHKTLSIDQDEFWASYDENBARFDPAVINFLQTKGOEKKYYGKSGQTGMGFA 195
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Db	121 TWSRANVYSPDSVSEWAFSDEKAYDLPATIDFIVQTKGOEKKHYGHSGQTGIFTA 180
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Qy	196 FSTMPBLAQKIKMFALATVKAHKSPOTKFLLPDMIKGLGKKEFL---YQTRFL 252
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Db	61 YRIPGKKNSEIGNGRPVAYLLHGIIASATWNLPNNSLAFIADGYDWLGNNSRGN 120
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Qy	136 AWSRKHKTLSIDQDEFWASYDENBARFDPAVINFLQTKGOEKKYYGKSGQTGMGFA 195
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Db	121 TWSRANVYSPDSVSEWAFSDEKAYDLPATIDFIVQTKGOEKKHYGHSGQTGIFTA 180
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Qy	196 FSTMPBLAQKIKMFALATVKAHKSPOTKFLLPDMIKGLGKKEFL---YQTRFL 252
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Db	61 YRIPGKKNSEIGNGRPVAYLLHGIIASATWNLPNNSLAFIADGYDWLGNNSRGN 120
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Qy	136 AWSRKHKTLSIDQDEFWASYDENBARFDPAVINFLQTKGOEKKYYGKSGQTGMGFA 195
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Db	121 TWSRANVYSPDSVSEWAFSDEKAYDLPATIDFIVQTKGOEKKHYGHSGQTGIFTA 180
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Qy	196 FSTMPBLAQKIKMFALATVKAHKSPOTKFLLPDMIKGLGKKEFL---YQTRFL 252
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Db	61 YRIPGKKNSEIGNGRPVAYLLHGIIASATWNLPNNSLAFIADGYDWLGNNSRGN 120
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Qy	136 AWSRKHKTLSIDQDEFWASYDENBARFDPAVINFLQTKGOEKKYYGKSGQTGMGFA 195
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Db	121 TWSRANVYSPDSVSEWAFSDEKAYDLPATIDFIVQTKGOEKKHYGHSGQTGIFTA 180
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Qy	196 FSTMPBLAQKIKMFALATVKAHKSPOTKFLLPDMIKGLGKKEFL---YQTRFL 252
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Db	61 YRIPGKKNSEIGNGRPVAYLLHGIIASATWNLPNNSLAFIADGYDWLGNNSRGN 120
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Qy	136 AWSRKHKTLSIDQDEFWASYDENBARFDPAVINFLQTKGOEKKYYGKSGQTGMGFA 195
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Db	121 TWSRANVYSPDSVSEWAFSDEKAYDLPATIDFIVQTKGOEKKHYGHSGQTGIFTA 180
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Qy	196 FSTMPBLAQKIKMFALATVKAHKSPOTKFLLPDMIKGLGKKEFL---YQTRFL 252
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Db	61 YRIPGKKNSEIGNGRPVAYLLHGIIASATWNLPNNSLAFIADGYDWLGNNSRGN 120
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Qy	136 AWSRKHKTLSIDQDEFWASYDENBARFDPAVINFLQTKGOEKKYYGKSGQTGMGFA 195
RA	RAXuehli P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,	Db</	

